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1 CGAGCCCGCAGCCGCCGCCGGCTCCTCTGGGATGTCCGTAGGACCCGGCCATTCAGGAC
                  NAME/KEY: CDS
LOCATION: (82)
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                SEQ ID NO 14
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Sequence 5, Appli
Sequence 15, Appl
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                                                           March 17, 2006, 10:45:07; Search time 2012 Seconds (without alignments) 6502.066 Million cell updates/sec
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Sequence 14, App
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Sequence 15, App
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Sequence 3, Ap
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Sequence 482,
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1: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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Biocceleration Ltd.
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US-10-305-720-1360
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Listing first 45 summaries
                                            - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Sequence 2448, Ap
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              Sequence
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### ALIGNMENTS

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OTHER INFORMATION: CRR-R splice-variant insert fragment inserted
OTHER INFORMATION: Detween nucleotides 516-517 of SEQ ID NO:1.
OTHER INFORMATION: /note= "This sequence is contained in clone
OTHER INFORMATION: "CRR-R2"."
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                                                                        JEAULICANT: CHEN', MATINI,

APPLICANT: Chen, Ruoping
APPLICANT: Lewie, Kathy A.
APPLICANT: Lewie, Kathy A.
APPLICANT: Lewie, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE REFERENCE: Salk1748
CURRENT APPLICATION NUMBER: US/09/191,724
CURRENT FILING DATE: 1998-11-12
BARLIER FILING DATE: 1998-01-17
EARLIER FILING DATE: 1998-01-17
EARLIER FILING DATE: 1994-02-9
EARLIER FILING DATE: 1993-06-25
EARLIER FILING DATE: 1993-06-25
EARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ for Windows Version 3.0
Sequence 14, Application US/09191724
Patent No. US20020055617A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 1582; Conservative
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ORGANISM: Homo sapiens
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	421 GTGCACTACCATGTCGCAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480 421 GTGCACTACCATGTCGCAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480 481 CTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGGCCAGCTGCATGGGGTGAC 540	
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                              961 GGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTGCTGATCAATTTC
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APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: CRF Receptor(8)
FILE REFERENCE: Salk1748
CURRENT APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-01-17
EARLIER FILING DATE: 1995-01-17
EARLIER PILING DATE: 1993-05-25
EARLIER FILING DATE: 1993-06-23
EARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. US20020055617A1
GENERAL INFORMATION:
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OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1. OTHER INFORMATION: /note= "This sequence is contained in clone OTHER INFORMATION: "CRF-R2"."
                                                                             Length 1582
                                                                                                          0; Indels
                                                                            DB 7;
                                                                          Query Match 100.0%; Score 1582; Best Local Similarity 100.0%; Pred. No. 0; Matches 1582; Conservative 0; Mismatches
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1054 ATCACCTACATGCTGTTCTTCGTCAATCCCCGGGGAGGATGAGGTCTCCCCGGGTCGTCTTC
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APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
ITLE OF INVENTION: Cloning and Recombinant Production of
ITILE OF INVENTION: CRF Receptor(s)
FILE REFERENCE: Salk1748
CURRENT APPLICATION NUMBER: US/10/649,193
CURRENT FILING DATE: 2002-082-26
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/191,724
PRIOR PILING DATE: EARLIER FILING DATE: 1998-11-12
PRIOR PILING DATE: EARLIER PILING DATE: 1998-01-17
PRIOR PLING DATE: EARLIER PILING DATE: 1955-01-17
PRIOR PLING DATE: EARLIER PILING DATE: US 08/374,009
PRIOR PLING DATE: EARLIER PILING DATE: US 08/353,537
                                                                                                                                             994 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGC
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Publication No. US20040039173A1
GENERAL INFORMATION:
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Pred. No. 0;
0; Mismatches 0; Indels 87
LENGTH: 1495
TYPE: DNA
OKGANISM: Homo sapiens
FRATURE:
NAME/KEY: CDS
LOCATION: (1326)
OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
OTHER INFORMATION: /note="This sequence is encoded by clone other Information: /note="This sequence is encoded by clone other Information: /core-R1"."
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Best Local Similarity 94.5%;
Matches 1495; Conservative
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Patent No. US20020142952A1
GENERAL INFORMATION:
APPLICANT: Genetics Institute, Inc.
APPLICANT: Wong, Gordon G.
APPLICANT: Fechtel, Kim
APPLICANT: Fechtel, Kim
APPLICANT: Applicant, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Resnick, Richard J.
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US-09-822-830A-30/c
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PRIOR FILING DATE: BARLIER FILING DATE: 1994-12-09
PRIOR PLING DATE: BARLIER FILING DATE: 1994-12-09
PRIOR FILING DATE: BARLIER FILING DATE: 1993-02-25
PRIOR FILING DATE: BARLIER FILING DATE: 1993-02-35
PRIOR PLICATION NUMBER: BARLIER APPLICATION NUMBER: US 08/110,286
PRIOR PLILOR DATE: BARLIER FILING DATE: 1993-06-18
PRIOR PLILOR DATE: BARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASESQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1495
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (82)...(1326)
OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
OTHER INFORMATION: /noce= "This sequence is encoded by clone"
OTHER INFORMATION: /noce= "This sequence is encoded by clone"
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Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87
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GENERAL INFORMATION:
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APPLICANT: Gulukota, Kamalakar
APPLICANT: Graham, James R.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REPERENCE: GIN 6402
CURRENT APPLICATION NUMBER: US/09/822,830A
CURRENT FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195,604
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 631
SOFTWARE: Patentin Ver: 2.0
ERNGTH: 2579
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88.4%; Score 1398; DB 3; Length 2579;

Best Local Similarity 94.5%; Pred. No. 0;

Matches 1495; Conservative 0; Mismatches 0; Indels 87
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US-09-822-830A-30
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Sequence 1. Application US/10649852

| Sequence 1. Application US/10649852
| Publication No. US20040101911A1
| GENERAL INFORMATION:
| APPLICANT: The Procter & Gamble Company
| APPLICANT: Beldon, Russell
| TITLE OF INVENTION: Methods for Identifying Compounds for Receptors
| TITLE OF INVENTION: Wethods for Identifying Compounds for Receptors
| TITLE OF INVENTION: Wethods for Identifying Compounds for Receptors
| TITLE OF INVENTION: Wethods for 1049,852
| CURRENT PILING DATE: 2003-08-27
| CURRENT PILING DATE: 2001-03-06
| NUMBER OF SEQ ID NOS: 44
| SOFTWARE: Patentin version 3.0
| SEQ ID NO 1
| LENGTH: 2536
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                                                             1019 GGGGGTGTACACCGACTACATCTACCAGGCCCCCATGATCCTGGTCCTGCTGATCATTTC
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                                                                                                                                   Score 1396.4;
Pred. No. 0;
0; Mismatches
                                                                                                                                   Query Match
Best Local Similarity 94.4%;
Matches 1494; Conservative
; TYPE: DNA
; ORGANISM: homo sapiens
; FRATURE:
; NAME/KEY: CDS
; LOCATION: (227)..(1474)
US-09-799-978-1
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8 6 8 6 8 6 8	61 GTCTCTGCCTCCTCCAGGACCAGCACTGCGAGAGCCTGTCCCTGGCCAGCAACATCTCA 120 202 GGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACCTGGCCCGCAGCCCTGCG 261 121 GGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACCTGGCTGG	Oy 1282 TCTGCCATCCGGAAGAGGTGGCA Db 1201 TCTGCCATCCGGAAGAGGTGGCA OY 1342 GCCGTGCCATGTCCATCCCAC OY 1261 GCCGTGCCATGTCCATCCCCCAC OY 1402 TCCACAGCATGTGA 1416 Db 1321 TCCACAGCAGTCTGA 1335	TCTGCCATCCGGAAGAGGTGGCACCGGTGGCACAGCACTCGATCCGTGCCCGAGTG 1341  TCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAGCACTCGATCCGTGCCCGAGTG 1341  TCTGCCATCCCGAAGAGGTGGCACCGGTGGCAGGACAAGCACTCGATCCGTGCCGAGTG 1260  GCCGTGCCATGTCCATCCCCACCTCCCCAACCCGTGTCAGCTTTCACAGCATCAAGCAG 1401  GCCCGTGCCATGTCCATCCCCACCTCCCCAACCCGTGTCAGCTTTCACAGCATCAAGCAG 1320  TCCACAGCAGTCTGA 1416  TCCACAGCAGTCTGA 1335
දු පු	GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCACTACCATGTCGCAGTC	RESULT 9 US-09-799-978-3 ; Sequence 3, Application US/09799978 ; Publication No. US20030165807A1	
<b>8</b> 8	ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCCTGGTGGCCTTTGTCCTC	; GENERAL INFORMATION: ; APPLICANT: The Procter & Gamble Company ; APPLICANT: Isfort, Robert ; APPLICANT: Sheldon, Russell	ompany
දි දි	502 ITTCTGGGGCTCAGGCTGCACCCATTGGGGTGACCAGGCAGTTGGAGCCCTGGAG 561		Identifying Compounds for Regulating Muscle Mass or g Corticotropin Releasing Factor Receptors 799,978
දි සි	562 GTGGGGGCTCCATGGAGTGCCCCATTTCAGGTTCGAAGGAGCATCCGGTGCCTGCGA 621	-	
සු දු	622 AACATCATCCACTGGAACCTCATCCTCGCGTACTCCTGCGCAACGCCACCTGGTTCGTG 681		
& g	682 GTCCAGCTAACCATGAGCCCCGAGGTCCACCAGAGCAACGTGGGGCTGGTGGAGGTTGGTG 741 	; FEATURE: CDS ; NAME/KEY: CDS ; LOCATION: (38)(1285) US-09-799-978-3	
<i>&amp;</i> ₽	742 ACAGCCGCTACAACTACTTCCATGTGACCAACTTCTTCTGGATGTTCGGCGAGGCCTGC 801	Query Match Best Local Similarity 93.7%; Pre Matches 1285; Conservative 0;	Score 1188; DB 3; Length 1285; Pred. No. 0; 0; Mismatches 0; Indels 87; Gaps 1;
දු පු	802 TACCTGCACACACCATGGTGCACCTACTCCACTGACCGGGTGCGCAAATGGATGTTC 861 11	Oy 45 CCCGGCATTCAGGACGTAGCC 	
è 8	862 AICTGCAITGGCTGGGGTGTGCCCTTCCCCAICAITGTGGCCCTTGGGAAGCTG 921	Oy 105 TCTCGTCAAGGCCCTTCTCCTTC	05 TCTCGTCAAGGCCCTTCTCCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCTCCAGGACCA 164
දු පු	922 TACTACGACAATGAGAAGTGCTGGTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATC 981 	Oy 165 GCACTGCGAGAGCCTGTGCCTGC	GCACTGCGAGAGCCTGTCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGT 224 
දු පු	982 TACCAGGCCCCATGATCCTGGTCTGGTGATTTCATCTTCCTTTTCAACATGGTC 1041	Oy 225 GGACCTCATTGGCACCTGCTGGC	GGACCTCATTGGCACCTGCTGGCACCCGCAGCGCAGCAGCTAGTGGTTCGGCCCTG 284
ò 8	1042 CGCATCCTCATGACCAAGCTCCGGGCATCCCACGTCTGAGACCATTCAGTACAGGAAG 1101 	Qy 285 CCCTGCCTTTTTCTATGSTGTCC 	CCCTGCCTTTTTCTATGGTGTCCCGCTACAAACAATGGCTACCGGGAGTGCCT 344
è 8	1102 GCTGTGAAAGCCACTCTGGTGCTGCCCCTCCTGGGCATCACCTACATGCTGTTCTTC 1161 1021 GCTGTGAAAGCCACTCTGGTGCTGCTGCTGCTCCTGGGCATCACCTACATGCTGTTCTTC 1080	Ay 345 GGCCAATGGCAGCTGGGCCCCC	GGCCAATGGCAGCCGCCGCCGCGTGAATTACTCCGAGTGCCAGGAGATCCTCAATGA 404 
& g	1162 GTCAATCCCGGGGGATGAGGTCTCCCGGGTCGTCTTCATCTACTTCAACTCCTTCTG 1221 1081 GTCAATCCCGGGGAGGATGAGGTCTCCCGGGTCGTCTTCACTTCAACTCCTTCTG 1140	Qy 405 GGAGAAAAAAGCAAGGTGCACT	ggagaaaaaaagcaaggrgcactaccargccaggcartarcaactaccrggggccactg 464 
<b>ራ</b> ብ	1222 GAATCCTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGT 1281 	Qy 465 TATCTCCCTGGTGGCCCTCCTGC 	TATCTCCCTGGTGGCCCTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGGCTG 524

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; Pred. No. 0;
0; Mismatches
CURRENT APPLICATION NUMBER: US/10/649,852
CURRENT FILING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 09/799,978
FRICH FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
EMOTH: 1285
TYPE: DNA
ORGANISM: HOMO Sapien8
                                                                                                                                                                                                                                   Query Match 75.1%;
Best Local Similarity 93.7%;
Matches 1285; Conservative (
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Publication No. US20040101911A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert
APPLICANT: Sheldon, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass of TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors
FILE REPERENCE: 8448R
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Db   694 CACCTACTCCACTGACCGGCAAATGGATGTTCATCTGCATTGGCTGGGGTGTGCC 753   Qy   885 CTTCCCCATCATTGTGGCCTTGGGAAGCTGTACTACGACAATGAGAAGTGCTG 944	CCTGCTGATCAATTTCATCTTTCAACATCGTCCGCATCCTCATGACCAAGGTCCGCGCTCCGCTCGCT	1125 GCTGCCCTCCTGGGCATCACCTACTGTTCTTCGTCAATCCCGGGAGGAT 1125 GCTGCCCTCCTGGGCATCACCTACTGTTCTTCGTCAATCCCGGGAGGAT 1125 GCTGCCCTCCTGGGCATCACCTACTGTTCTTCGTCAATCCCGGGAGGAT 1185 CTCCCGGGTCGTTCATCTACTTCAACTCCTTCCTGAATCCTTCCAGGGCTTC 1185 CTCCCGGGTCGTTCATCTACTTCAACTCCTTCCTGAATCCTTCCAGGGCTTC 11054 CTCCCGGGTCGTTCATCTACTTCAACTCCTTCCTGAATCCTTCCAGGGCTTC	Qy 1245 GTCTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAAGAGGTGGCA 1304		S-10-450-097-30 Sequence 30, Application US/10450097 Sequence 30, Application US/10450097 Publication No. US20040110252A1 GENERAL INFORMATION: APPLICANT: Septegen Ltd TITLE OF INVENTION: Yeast-Based Assay FILE REFERENCE: DE/p701948PCT CURRENT APPLICATION NUMBER: US/10/45C CURRENT FILING DATE: 2003-05-29	PRIOR APPLICATION NUMBER: GB 0030038.4 PRIOR FILING DATE: 2000-12-08 NUMBER OF SEQ ID NOS: 53 SOFTWARE: PATENTIN Ver. 2.1 SEQ ID NO 30 LENGTH: 10042	interioral Sequence CRGANISM: Artificial Sequence FEATURE: COTHER INFORMATION: Description of Artificial Sequence:pREPXr-CRHR US-10-450-097-30	Duery Match  73.0%; Score 1154.2; DB 7; Length 10042;  6est Local Similarity 93.3%; Pred. No. 5.4e-310;  Matches 1253; Conservative 0; Mismatches 3; Indels 87; Gaps  75 CCCGAAGAAGAACACCCGCAACTCCGTCTCGTCAAGACCTTCTCTTCTGGGGTT	DD 1227 CTCTAGAANGGGAGCCCGCAGCTCCGCAGGCCCTTCTCCTTCTGGGGCCT 1286 QY 135 GAACCCCGTCTCCTCCCTCCAGGACCAGCACTCCGGAGAGCCTGTCCCTGGCCAGCAA 194 DD 1287 GAACCCCGTCTCTGCCTCCTCCAGGACCAGCAGAGAGCCTGTCCCTGGCCAGCAA 1346

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Sequence 482, Application US/09826509
Sequence 482, Application US/09826509
Publication No. US20030204073A1
SEQUENCE INFORMATION:
APPLICANT: Liaw, Chen W.
APPLICANT: Liaw, Chen W.
TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
TITLE OF INVENTION: Protein-Coupled Receptors
TITLE OF INVENTION: US/09/826,509
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 72.8%; Score 1151; DB 7;
Best Local Similarity 93.5%; Pred. No. 2.4e-309;
Matches 1248; Conservative 0; Mismatches 0;
                                                                                                                                                                                                               RESULT 12
US-10-450-097-28

Sequence 28, Application US/10450097
FUDLICATION NO. US20040110252A1
GENERAL INFORMATION:
TITLE OF INVENTION: Yeast-Based Assay
FILE REFERENCE: DE/P701948PCT
CURRENT APPLICATION NUMBER: US/10/450,097
CURRENT FILING DATE: 2003-05-29
FRIOR PILING DATE: 2000-12-08
NUMBER OF SEQ ID NOS: 53
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 28
LENGTH: 1248
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1174 GCCCGTGCCATGTCCATCCCCACCTCCCCAACCAGCTGTCAGCAGCAGCAG
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; Bublication No. US20050019840A1
; GRENEAL INFORMATION:
    APPLICANT: Liaw, Chen W.
    APPLICANT: Liam, I-Lia
    TITLE OF INVENTION: Non-Endogenous, Constitutively Activated Known G
    TITLE OF INVENTION: NON-Endogenous, Constitutively Activated Known G
    TITLE OF INVENTION: NON-Endogenous, Constitutively Activated Known G
    TILL REFERENCE: AREN-207
    CURRENT APPLICATION NUMBER: US/10/925,095
    CURRENT FILING DATE: 2004-00-24
    PRIOR PILING DATE: 2004-07
    PRIOR APPLICATION NUMBER: 09/170,496
    PRIOR APPLICATION NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAATCCTTCCAGGCTTCTTTGTGTCTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGT
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                                                                                                                                                                                                               1102 GCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTGGGCATCACCTACATGCTGTTCTTC
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Best Local Similarity 93.4%; Pred. No. 6.7e-309;
Matches 1247; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1234 TCCACAGCAGTCTGA 1248
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US-10-925-095-482
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                                                                                                                                                                                                                                                                                                                                                             82 ATGGGAGGCACCCGCAGCTCCGTCTAAGGCCCTTCTCCTTCTGGGGCTGAACCCC 141
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                                                                                                                                                                                                                                                                                                                                                                                               1 ATGGAAGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTTCTCCTTCTGGGGCTGAACCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 202 GGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACCTGCTGGCCCCCGCAGCCCTGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 GGGCAGCTAGTGGCTTCGGCCCTGCCTTTTTCTATGGTGTCCGCTACAATACCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCCTGGTGGCCTTTGTCCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               361 ATCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCCCTCCTGGTGGCCCTTTGTCCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                862 ATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCTGGGCCATTGGGAAGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 TACTACGACAATGAGAAGTGCTGGTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAGCAAGGTGCACTACCATGTCGCAGTC
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                                                                                                                                                                                                                                                                                                     87; Gaps
                                                                                                                                                                                                                                    Score 1149.4; DB 3; Length 1248; Pred. No. 6.7e-309; 0; Mismatches 1; Indels 87;
NUMBER OF SEQ ID NOS: 589
SOFTWARE: Patentin Version 2.1
SEQ ID NO 482
LENGTH: 1248
                                                                                                                                                                                                                                    Query Match
Best Local Similarity 93.4%;
Matches 1247; Conservative
                                                                                                                     ; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 Trrcreceerc
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AACATCATCCACTGGAACCTCATCTCCGCCTTCATCCTGGGCAACGCCACCTGGTTCGTG 681	2 GTCCAGCTAACCATGAGCCCCGAGGTCCACCAGAGCAACGTGGGGCTGGTGCAGGTTGGTG	e (1		2 TACCTGCACACACCCTCGTGCTACTACTCCACTGACGGGTGCGAAATGGATGTTC 861	4	2 ATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCTGGGCCATTGGGAAGCTG 921		2 TACTACGACAATGAGAAGTGCTGGTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATC 981	-	2 TACCAGGGCCCATGATCCTGGTCCTGATCAATTTCATCTTTCTT	4	2 CGCATCCTCATGACCAAGCTCCGGGCATCCACCACGTCTGAGACCATTCAGTACAGGAAG 1101	4	2 GCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGCATCACCTACATGCTGTTCTTC 1161	₹*	2 GTCAATCCCGGGGAGGATGAGGTCTCCCCGGGTCGTCTTCATCTACTTCAACTCCTTCCT	4	2 GAATCCTTCCAGGGCTTCTTTGTGTCTGTTCTACTGTTTCCTCAATAGTGAGGTCCGT 1281	4	2 TCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAGCACTCGATCCGTGCCCGAGTG 1341		2 GCCCGTGCCATGTCCATCCCCACCTCCCCAACCCGTGTCAGCTTTCACAGCATCAAGCAG 1401	O	2 TCCACAGCAGTCTGA 1416	N
622	99	74.	574	802	63,	862	694	923	754	982	81,	104	87,	1102	93,	1162	66	1223	105	1283	1072	134	113	1402	1193
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Search completed: March 17, 2006, 12:51:02 Job time : 2017 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on:

March 17, 2006, 10:35:52; Search time 389 Seconds (without alignments) 7229.055 Million cell updates/sec

US-10-649-193-14 Title: Perfect score:

1582

1 cgagcccgcagccgcccgcc.....gctctccccctgcagccgtg 1582 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

1303057 segs, 888780828 residues Searched:

2606114 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

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./cgn2\_6/ptodata/1/ina/PP\_COMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result		Query				-
۱. ا	Score	Match	Length DB	8	ID	Description
-	1582	100.0	1582	4	US-08-482-746-14	Sequence 14, Appl
F	1582	100.0	1582	٣	US-09-580-734-14	Sequence 14, Appl
m	1582	100.0	1582	ო	US-08-374-009-14	Sequence 14, Appl
F	1387	100.0	1582	r	-8S-09-191-724-14	Sequence 14, Appl
ß	1398	88.4	1495	٣	US-08-482-746-1	Seguence 1, Appli
9	1398	88.4	1495	٣	US-09-'580-734-1	H
7	1398	88.4	1495	٣	US-08-374-009-1	Sequence 1, Appli
æ	1398	88.4	1495	٣	US-09-191-724-1	ī
6	1396.4	88.3	2536	e	US-09-799-978-1	٦,
10	1335	84.4	1335	٣	US-09-016-434-1360	136
11	1283	81.1	1380	~	US-08-110-286A-1	Sequence 1, Appli
12	1188	75.1	1285	h	US-09-799-978-3	Sequence 3, Appli
13	1149.4	72.7	1248	m	US-09-826-509-482	Sequence 482, App
14	1057	9.99	1206	e	US-09-799-978-7	
12	1035.2	65.4	1411	m	US-08-482-746-5	Sequence 5, Appli
16	1035.2	65.4	1411	ო	US-09-580-734-5	Sequence 5, Appli
17	1035.2	65.4	1411	٣	US-08-374-009-5	2,
18	1035.2	65.4	1411	٣	US-09-191-724-5	'n
19	1035.2	65.4	1411	m	US-09-799-978-15	15,
20	1013.4	64.1	1248	m	US-09-799-978-39	39,
21	1006.8	63.6	2273	٣	US-09-799-978-21	21,
22	1003.8	63.5	1248	ო	US-09-799-978-27	Sequence 27, Appl
23	196	119	1248	7	US-08-110-286A-5	S,
47	919	58.1	1146	r	08-09-799-978-5	'n,

22 3 US-09-799-978-41 42 3 US-09-799-978-35 48 3 US-09-799-978-35 58 3 US-09-799-978-11 58 2 US-08-799-978-11 58 2 US-08-381-433-7 10 3 US-09-981-401-7 10 3 US-09-978-978-978-9 56 2 US-08-381-433-1 56 2 US-08-381-433-1 56 3 US-09-978-978-9 56 3 US-09-978-178-17 56 3 US-09-981-401-1 14 2 US-08-881-401-1 14 3 US-09-978-978-978-17 14 3 US-09-978-978-17 14 3 US-09-978-178-17 17 3 US-09-978-178-17 18 3 US-09-789-978-19 18 3 US-09-789-978-19 18 3 US-09-789-978-19 18 3 US-09-789-978-19 18 3 US-09-789-978-19 18 3 US-09-789-978-19	Sequence 11, Appl Sequence 33, Appl Sequence 29, Appl Sequence 21, Appl Sequence 7, Appli Sequence 1070, Appli Sequence 13, Appli Sequence 13, Appli Sequence 13, Appli Sequence 1, Appli Sequence 19, Appli Sequence 9, Appli
0.000000000000000000000000000000000000	US-09-799-978-41 US-09-799-978-35 US-09-799-978-35 US-09-799-978-35 US-09-799-978-11 US-08-381-433A-7 US-09-881-401-7 US-09-978-13 US-09-978-13 US-09-799-978-13 US-09-799-978-13 US-09-799-978-13 US-09-799-978-13 US-09-799-978-13 US-09-799-978-13 US-09-799-978-13 US-09-881-401-13 US-09-881-401-13 US-09-981-401-13 US-08-981-401-13
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### ALIGNMENTS

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NAME/KEY: CDS

LOCATION: (82)...(1413)

LOCATION: (82)...(1413)

COTHER INFORMATION: CRF-R splice-variant insert fragment inserted

COTHER INFORMATION: Detween nucleotides 516-517 of SEQ ID NO:1.

COTHER INFORMATION: CRF-RE"."

CTHER INFORMATION: "CRF-RE"."
   TYPE: DNA
ORGANISM: Homo sapiens
US-08-482-746-14
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0; Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 0;,
Matches 1582; Conservative 0; Mismatches 0; Indels 0;

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1 CGAGCCGCAGCCGCCCGCTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC

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1141 ATCACCTACATGCTGTTCTTCGGGGGGGGGGGGGTCCCCGGGTCGTTCT	NESULT 2  US-5580-734-14  US-5580-734-14  US-560-580-734-14  Sequence 14, Application US/09580734  PEREIN No. 6402608  GRNERAL INPORMATION: APPLICANT: Chen, Ruoping APPLICANT: Sawchenko, Paul TITLE OF INVERTION: Chen, Wylte W. TITLE OF INVERTION: Chen, Paul TITLE OF THE TITLE OF THE TIPL OF THE TIPL TITLE OF THE TIPL OF THE TIPL TITLE OF THE TIPL TITLE OF THE TIPL TIPL TITLE OF THE TIPL TITLE OF THE TIPL TIPL TITLE OF THE TIPL TIPL TIPL TIPL TIPL TIPL TIPL TIPL
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                                                       1081 GAGACCATTCAGTACAGGAGGCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGC
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APPLICANT: Chen, Racilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Lewie, Kathy A.
APPLICANT: Lewie, Kathy A.
APPLICANT: Danaladon, Cynthia J.
APPLICANT: Bawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of TITLE REFERENCE: P41 9886
CURRENT APPLICATION NUMBER: US 08/353,537
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1994-12-09
EARLIER APPLICATION NUMBER: US 08/110,286.
EARLIER APPLICATION NUMBER: US 08/110,286.
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1994-05-25
EARLIER FILING DATE: 1994-05-25
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 1582
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US-08-374-009-14
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                                                                                                                     Gaps
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   ; OTHER INFORMATION: /note= "This sequence is contained in clone; OTHER INFORMATION: "CRF-R2"."
US-09-580-734-14
                                                                                Length 1582
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                                                                              Score 1582;
Pred. No. 0;
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                                                                              Query Match
Best Local Similarity 100.0%;
Matches 1582; Conservative 0
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                                    901 GCCTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGCTGGTTTGGCAAAAAGGCCT
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               GCCTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGCTGGTTTGGCAAAAAGGCCT
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Patent No. 6638905

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Derrin, Marilyn H.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldeon, Cynthia J.
APPLICANT: Sawchenko, Paul
ITLE OF INVENTION: Cloning and Recombinant Proj
ITLE OF INVENTION: Cloning and Recombinant Proj
ITLE OF INVENTION: Cloning and Recombinant Proj
ITLE OF INVENTION: Cloning and Receptor(8)
FILE REFERENCE: Salk1148
CURRENT FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-01-17
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1991-05-25
EARLIER FILING DATE: 1993-05-25
EARLIER PELING DATE: 1993-05-25
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     PERTURE:
NAME/KEY: CDS
COCATION: (82)...(1413)
COCATION: (82)...(1413)
OTHER INFORMATION: CR-R splice-variant insert fragment inserted
OTHER INFORMATION: between nucleotides 516-517 of SEQ ID NO:1.
OTHER INFORMATION: /note= "This sequence is contained in clone
OTHER INFORMATION: "CRP-R2"."
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b; Pred. No. 0;
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Best Local Similarity 100.0%;
Matches 1582; Conservative 0;
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Patent No. 6399315

GENERAL INFORMATION:

APPLICANT: Pertrin, Marilyn H.

APPLICANT: Chen, Ruoping

APPLICANT: Usewis, Kathy A.

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APPLICANT: Donaldson, Cynthia J.

APPLICANT: Sawchenko, Paul

TITLE OF INVENTION: Cloning and Recombinant Production of

TITLE OF INVENTION: Cloning and Recombinant Production of

TITLE OF INVENTION: CRP Receptor (8)

FILE REPERENCE: P41-90002

CURRENT APPLICATION NUMBER: US/08/482,746B
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BARLIER FILING DATE: 1993-08-23

BARLIER APPLICATION NUMBER: US 08/079,320

EARLIER PILING DATE: 1993-06-18

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SOTTWARE: PastSEQ for Windows Version 3.0

TYBE: DNA

ORGANISM: Homo sapiens

FRATURE:

NAME/KEY: CDS

LOCATION: (82)...(1413)

OTHER INFORMATION: CRF-R splice-variant insert fragment inserted

OTHER INFORMATION: Detween nucleotides 516-517 of SEQ ID NO:1.

OTHER INFORMATION: "CRF-R in sequence is contained in clone

US-09-191-724-14
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; Pred. No. 0;
0; Mismatches
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Best Local Similarity 100.0%;
Matches 1582; Conservative 0
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                                                                                                                                                           TGGATGTTCGGCGAGGCTGCTACCTGCACACACCCATCGTGCTCACCTACTCCACTGAC
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                                                                                GTGGGCTGGTGCAGGTTGGTGACAGCCGCCTACAACTACTTCCATGTGACCAACTTCTTC
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Patent No. 6482608
GENERAL INFORMATION
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 88.4%; Score 1398; DB 3; Length 1495; Best Local Similarity 94.5%; Pred. No. 0; Makches 1495; Conservative 0; Mismatches 0; Indels 87
                                                                                                                                                                                                                                                                                                                                FEATURE:
| NAME/KRY: CDS
| LOCATION: (81)...(1326)
| OTHER INFORMATION: /product = "Human pituitary CRF-receptor"
| OTHER INFORMATION: /note= "This sequence is encoded by clone US-08-482-746-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EARLIER PELING DATE: 1995-01-17
EARLIER PILING DATE: 1995-01-17
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EARLIER PILING DATE: 1994-12-09
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EARLIER PILING DATE: 1994-05-25
EARLIER PILING DATE: 1993-08-23
EARLIER PILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-08-18
NUMBER OF BEQ ID NOS: 15
SOFTWARE: PREUSER FILING DATE: 1993-06-18
NUMBER OF BEQ ID NOS: 15
SOFTWARE: PREUSER FILING DATE: 1993-06-18
NUMBER OF BEQ ID NOS: 15
SOFTWARE: PREUSER FILING DATE: 1993-06-18
NUMBER OF BEQ ID NOS: 15
SOFTWARE: PREUSER FILING DATE: 1993-06-18
FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Homo sapiens
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APPLICANT: Bonaldson, Cynthia J.
FAPLICANT: Sawchenko, Paul
TITLE OF INVENTION: CRF Receptor(s)
FILE REPREBERGE: Salk1748
CURRENT APPLICATION WUMBER: US/09/580,734
CURRENT PILING DATE: 1090-10-26
FRIOR APPLICATION NUMBER: US 08/374,009
FRIOR FILING DATE: 1998-11-12
FRIOR PELING DATE: 1998-11-12
FRIOR PELING DATE: 1998-11-20
FRIOR FILING DATE: 1998-11-20
FRIOR FILING DATE: 1993-10-27
FRIOR PELING DATE: 1993-10-25
FRIOR FILING DATE: 1993-06-25
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Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEATURE:
NAME/KEY: CDS
LOCATION: (82)...(1326)
COCATION: (Product = "Human pituitary CRF-receptor"
OTHER INFORMATION: /note= "This sequence is encoded by clone
OTHER INFORMATION: (RCRF-RI","
                                                                                                     GENERAL INCOMENTATION:

GENERAL INCOMENTATION:

APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.

APPLICANT: Denaidson, Cynthia J.

APPLICANT: Donaidson, Cynthia J.

APPLICANT: Sawchenko, Paul
ITILE OF INVENTION: Cloning and Recombinant Production of
ITILE OF INVENTION: Cloning and Recombinant
FILE REFERENCE: P41 9866

CURRENT APPLICATION UNMER: US 08/374,009A

CURRENT APPLICATION NUMBER: US 08/353,537

EARLIER FILING DATE: 1994-10-10

EARLIER PILING DATE: 1994-0-18

EARLIER PILING DATE: 1994-0-23

EARLIER PILING DATE: 1993-08-23

EARLIER PILING DATE: 1994-05-25

NUMBER OF SEQ ID NOS: 15

SQTWARE: FRESEQ for Windows Version 3.0

SEQ ID NO 1

LENGTH: LASS
                                                   Sequence 1, Application US/08374009A Patent No. 6495343 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                     -08-374-009-1
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                                                                                                                                                                                       GENERAL INCORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Danaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: CRF Receptor(8)
TITLE OF INVENTION: CRF Receptor(8)
TITLE OF INVENTION: CRF Receptor(8)
TITLE OF INVENTION: Salk1748
CURRENT APPLICATION NUMBER: US 08/191,724
CURRENT FILING DATE: 1998-11-17
EARLIER FILING DATE: 1994-10-17
EARLIER FILING DATE: 1994-09-29
EARLIER FILING DATE: 1993-05-25
EARLIER FILING DATE: 1993-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA

ORGANISM: Homo sapiens

PEATURE:

NAME/KRY: CDS

LOCATION: (82)...(1326)

OTHER INFORMATION: /product = "Human pituitary CRF-receptor"

OTHER INFORMATION: /note= "This sequence is encoded by clone

US-09-191-724-1
                         1474 CCGCTCTCCCCTGCAGCCGTG 1495
                                                                                                                                                      Sequence 1, Application US/09191724
Patent No. 6638905
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481 CTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCCATTGGGGTGAC 540 [1	CGCAACGCCACCTGGTTCGTGGTCCAGCTAACCATGAGCCCCCGAGGTCCACCCAGAGCAAC  GGCAACGCCACCTGGTTCGTGGTCCAGCTAACCATGAGCCCCGAGGTCCACCCAGAGCAAC  GTGGGTGGTGGTGGTTGGTGACAGCCGCCTACAACTTCCATGTGACCAACTTCTTC  GTGGGTGGTGCAGGTTGGTGACAGCCGCCTACAACTTCCATGTGACCAACTTCTTC  TGGATGTTCGGGGTGGTTGGTGACAGCCGCTACAACTTCCATGTGACCAACTTCTTC  TGGATGTTCGGCGAGGGTTGCTACCTGCACACACGCCATCGTGATCTTCTTC  TGGATGTTCGGCGAGGGTTGCTACCTGCACACACGCCATCGTGCTCACTTCTTCTTC  TGGATGTTCGGCGAATGGTTACATCGCAACACACGCCATCATTGTG  GGGTTGTACACCAACACAACA	1021 ATCTTCTTTTCAACATCGTCATCATCATCACCAGCTCCGGGCATCCACGTCT   1080
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Qy         1441 CAAAGAGCTGTGGCGGGGGAATGACGGCCAGGCTCCTGACCACCTGTGGAGGT 1500           Db         1354 CAAAGAGCTGTGGCTGGGGGGAATGACGGCTCGTGCTGTGCTGTGGAGGT 1413           Qy         1501 GACCTGTTAGGTCTCCATGCCCACCTGCCTGCCTGCTGGAGGT 1413           Db         1414 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCTGGCACTGACAGCTTGAGGGGG 1560           Db         1414 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCTGGCTG	RESULT 9 US-09-798-1 is Sequence 1, Application US/09799978 sequence 1, Application US/09799978 sequence 1, Application US/09799978 sequence 1, Application US/09799978 sequence 1, Application US/0979978 sequence 2, Application Sequence 2, Application Sequence 3, APPLICANT: Tiefort, Robert 3, APPLICANT: Tiefort, Robert 3, APPLICANT: Sheldon, Russell 3, TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle 3, TITLE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors 7, TITLE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors 5, CURRENT FILING DATE: 2001-03-06 NUMBER OF SEQ ID NOS: 44 sequence 2, Application 3.0 sequence 2, Application 3.0 sequence 2, Application 3.0 sequence 2, Application 3.0 sequence 3, Application 3.0 sequence 4, Application 3.0 sequence 5, Application 3.0 sequence 6, Application 3.	Query Match         88.34; Score 1396.4; DB 3; Length 2536;           Best Local Similarity         94.44; Pred. No. 0;           Matches 1494; Conservative         0; Mismatches         1; Indels 87; Gaps         1;           dy         1 conservative         0; Mismatches         1; Indels 87; Gaps         1;           dy         1 cadaccccacaccaccaccaccaccaccaccaccaccacc

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1261 GCCCGTGCCATGTCCATCCCCACCTCCCCAACCGGTGTCAGGCTTTCACAGCATGAAGAG 1320
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                                                                                                              301 GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAGGTGCACTACCATGTCGCAGTC
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1402 TCCACAGCAGTCTGA 1416
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: Mord Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
APPLICATION:
APPLICATION:
APPLICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
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                                                                                                                              Sequence 1366, Application US/09016434

Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Jeffrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECT
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
84.4%; Score 1335; D
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1335; Conservative 0; Mismatches
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TELECOMMUNICATION INFORMATION:
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1360:
SEQUENCE CHARACTERISTICS:
LENGTH: 1335 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
1619 CGCTCTCCCCTGCAGCGTG 1640
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FIMEDIATE SOURCE:
ILIBRARY: GENBANK
CLONE: 9408691
US-09-016-434-1360
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STATE: CALIFORNIA
COUNTRY: USA
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                   TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACC
                                        241 TGCTGGCCCCGCAGCCCTGCGGGGCAGCTAGTGGTTCGGCCCTGCCCTGCCTTTTTCTAT
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CRF-RECEPTOR"
/note= "This sequence is encoded by clone
"CRF-R1"."
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81.1%; Score 1283; DB 2; Length 1380;
Best Local Similarity 94.1%; Pred. No. 4.8e-314;
Matches 1380; Conservative 0; Mismatches 0; Indels 87
                                                                               Sequence 1, Application US/08110286A

Patent No. 5728545

GENERAL INFORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen's Ruchy A.
APPLICANT: Used Jr., Wylle W.
APPLICANT: Used Jr., Wylle W.
APPLICANT: Ostale Jr., Wylle W.
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF TITLE OF INVENTION: CRP RECEPTOR(S)
WUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/110,286A

FILING DATE:
                                                                                                                                                                                                                                                              JUNESSEE: Pretty, Schroeder, Brueggemann & (STREET: 444 South Flower Street, Suite 2000 CITY: Los Angeles STATE: CA COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Relter, Stephen E.
REGIGTRATION NUMBER: 31,192
REPRENCE/DOCKET NUMBER: P41 9439
TELEPHONE: 619-546-4737
TELEPHONE: 619-546-4737
INPORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,320
FILING DATE: 18-UDN-1993
ATTORNEY/AGENT INFORMATION:
1321 TCCACAGCAGTCTGA 1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1380 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
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LOCATION: 82..1329
OTHER INFORMATION: /
OTHER INFORMATION: COTHER INFORMATION: /
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                                                        RESULT 11
U8-08-110-286A-1
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Qy         465 TATCTCCCTGGTGGCCTCCTGGTGGCCTTTTGTCCTCTTTTCTGCGGCTCAGGCTG 524	Qy 525 CACCCATTGGGGTGACCAGGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGC 584  Db 470	Oy 585 CCCATTTCAGGTTCGAAGGACATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCAT 644	Oy 645 CTCCGCCTTCATCCTGCGCAACGCCACCTGGTTCGTGGTTCCAGCTAACCATGAGCCCCGA 704	QY         705         GGTCCACCACAACGTAGGTGCAGGTTGGTGACAGCCGCCTACAACTACTTCCA         764           Db         574         GGTCCACCAGAGCAACGTGGGCTGCAGGTTGGTGACAGCCGCCTACAACTACTTCCA         633	QY         765 TGTGACCAACTTCTTCTGGATGTTCGGCGAGGCTGCTACCTGCCACCACCACCGGCTTCGTGCT         824           Db         634 TGTGACCAACTTCTTCTGGATGTTCGGCGAGGCTGCTACCTGCACCACCACCGTGCTTCGTGCT         693	Qy 825 CACCTACTCCACTGACCGGCTGCGCAAATGGATGTTCATCTGCATTGGCTGGGGTGTGCC 884	QY         885         CTTCCCCATCATTGTGGCCTCGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGCTG         944           DD         754         CTTCCCCATCATTGTGGCCTTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGCTG         813	QY         945 GTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGT         1004           Db         814 GTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGT         873	Qy 1005 CCTGGTGATCAATTTCATCTTTCAACATCGTCGGCATCCTCATGACCAAGCTCCG 1064	OY 1065 GGCATCCACCACGTCTGAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCT 1124	Qy 1125 GCTGCCCTCCTGGGCATCACTACATGCTGTTCTTCGTCAATCCCGGGGAGGATGAGGT 1184	Qy 1185 CTCCCGGGTCGTCTTCATCTACTTCAACTCCTTCCTGGAATCCTTCCAGGGCTTCTTGT 1244	GICTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGGTGGCA 	Oy 1305 CCGTGGCAGACAAGCACTCGATCCGTGCCCAGTGGCCCGTGCCATGTCCATCCCCAC 1364	Oy 1365 CTCCCCAACCCGTGTCAGCTTTCACAGCAGTCAGAGTCTGA 1416	RESULT 13 US-09-826-509-482 ; Sequence 483, Application US/09826509	; FACELLANT: DOUGHATION: ; APPLICANT: Lehmann-Bruinsma, Karin ; APPLICANT: Liaw, Chen W. ; APPLICANT: Lin, I-Lin
Qy         1261 TICCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320           Db         1174 TICCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1233	Qy         1321 CACTCGATCGGGGCCGGGGCCGTGCCATGTCCATCCCCCACCCCGACCCGTGTC 1380           Db         1234 CACTCGATCGCCGGGTGGCCCGTGCCATGTCCATCCCCACCCCCCACCCGTGTC 1293	QY         1381 AGCTTTCACAGCACTCCACAGCAGTCTGAGCTGGCAGGCCATCTGAGCAGCCCC         1440           Db         1294 AGCTTTCACAGCATCAAGCAGCTCTGAGCTGGCAGCTCATGGAGCAGCCCC         1353	Qy         1441 CAAAGACTGTGGCTGGGGGGATGACG         1467           Db         1354 CAAAGACTGTGGGGGGATGACG         1380	RESULT 12 US-09-799-978-3	Sequence 3, 2 Patent No. 6 GENERAL INFO APPLICANT:	APPLICANT: Sheldon, Russell APPLICANT: Sheldon, Russell IIILE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or ITILE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors	CURRENT APP CURRENT FIL	; SOFTWAKE: Patentin Version 3.0 ; SEQ ID NO 3 ; TYPE: DNA	) OKKANILSM: HOMO BADIENB ) FEATURE: ) NAME/KEY: CDS ); LOCATION: (38)(1285)	Query Match Best Local Matches 128	GGTAGCGAGGAGCCGAGGATGGGAGGGCACCCGCAGCTCCG 10	105 TCTCGTCAAGGCCCTTCTCCTTCTGGGGCCCTGAACCCCGGTCTCTGCCTCCTCCGGGACCAGTCTTTTTTCTTCTTCTTCTTTTTTTT	165 GCACTGCGAGAGCCTGTGGCCACCACACACACACGCATGCAGTGCAACGCATCCGT	Qy         225 GGACCTCATTGGCACCTGCTGCACCCTGCGGGGCCAGCTAGTGGTTCGGCCCTG         284           Db         181 GGACCTGTTTGGCACTGCTGCTGCTGCAGCCTGCGGGGCTAGTTCGGCCTG         240	285 CCCTGCCTTTTTCTATGGTGTCCGCTACAATACCACAAACGGTACCGGGAGTGCCT 	Oy 345 GGCCAATGGCAGCTGGGCCGCGTGAATTACTCCGAGTGCAGGAGATCCTCAATGA 404	OY 405 GGAGAAAAAGCAAGGTGCACTACCATGTCGCAGTCATCAACTACCTGGGCCACTG 464

us-10-649-193-14.rni

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Sequence 7, Application US/09799978
Patent No. 6670140
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Sheldon, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass of TITLE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors
FILE REPERENCE: 8448
CURRENT APPLICATION NUMBER: US/09/799,978
CURRENT PILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
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                                 CGCATCCTCATGACCAAGCTCCGGGCATCCACCACGTCTGAGACCATTCAGTACAGGAAG
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ORGANISM: Homo sapiens
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US-09-799-978-7
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TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known TITLE OF INVENTION: Protein-Coupled Receptors FILE REFERENCE: AERN-207
CURRENT APPLICATION NUMBER: US/09/826,509
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 60/195,747
PRIOR APPLICATION NUMBER: 09/170,496
PRIOR FILING DATE: 1998-10-13
NUMBER OF SEQ ID NOS: 589
SOFTHARE: Patentin Version 2.1
SEQ ID NO 482
LENGTH: 1248
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Pred. No. 2.4e-280;
0; Mismatches 1; Indels 87;
                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 93.4%;
Matches 1247; Conservative (
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
US-09-826-509-482
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	RESULT 15 US-08-482-746-5  i Sequence 5, Application US/08482746B  patent No. 6399315  GENERAL INFORMATION: APPLICANT: Chen, Ruoping APPLICANT: Chen, Ruoping APPLICANT: Lewis, Kathy A. APPLICANT: Vale Jr., Wylie W. APPLICANT: Sawchenko, Paul ITILE OF INVENTION: CRF Receptor(8) FILLE REFERENCE: P41-90002 CURRENT APPLICATION NUMBER: US/08/482,746B  CURRENT PILING DATE: 1995-06-07 CURRENT PILING DATE: 1995-06-07 CURRENT PILING DATE: 1995-06-07	### AFALLER PILING DATE: 1995-01-17  ### AFALLER PILING DATE: 1994-12-09  ### AFALLER PILING DATE: 1994-12-09  ### AFALLER PILING DATE: 1994-12-09  ### AFALLER PILING DATE: 1994-05-25  ### AFALLER PILING DATE: 1993-06-25  ### AFALLER PILING DATE: 1993-06-25  ### AFALLER PILING DATE: 1993-06-18  ### APALLER	NAMB/KERT: CDS   NAMB/KERT: CDS	Db 181 CCTGACCAGCAATGTTTCTGGCCTGCAGTGCATCCGTGGACCTCATTGGCACCTG 240
142 GTCTCTGCCTCCAGGACCAGCACTGCGAGGGCCTGTCCCTGGCCAGCAACATCTCA 201  [		### ### ##############################		GAATCCTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGT

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301	TGTCCGCTACAACACGACAAACAATGGCTACCGGGAGTGCCTGGCCAACGGCAGCTGGGC 36	ò	144
363	CGCCCCCTGAATTACTCCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAGGCAAGGT 422 	qq	135
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421	ACACTACCATGTTGCAGTCATCATCAACTACCTGGGTCACTGCATCTCCCTGGTAGCCT	qq	141
483		Search Job ti	rch compl time : 3
543	GGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGGTGCTGCCCCATTTCAGGTTCGAAG		
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603 514	GAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCCGGCTTCATCCTGCG 662		
663 574	CAACGCCACTGGTTCGTGGTCCAGCTAACCATGAGCCCCCAGGTCCACCAGGAACGT 722		
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783 694	GATGTTCGGCGAGGGCTGCTACCTGCACACACCATCGTGCTCACCTACTCCACTGACCG 842 		
843 754	GCTGCGCAAATGGATGTTCATCTGCATTGGCTGGGGGTGTGCCCTTCCCCATCATTGTGGC 902 		
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1083	GACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGCAT 1142		
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1203	CTACTTCAACTCCTTCCTGGAATCCTTCCAGGCTTCTTTGTGTCTGTGTTCTACTGTTT 1262 		
1263	CCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAGCA 1322 		
1323	CTCGATCCGTGCCCGAGTGGCCCGTGCCATGTCCCACCTCCCCCAACCCGTGTCAG 1382		

qq	1234		1293
ò	1383	1383 CTTTCACAGCATCAAGAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCCCCA 1442	1442
q	1294	1294 CTTTCACAGCATCAAGCAGTCCACAGTGTGAGCT-CCAGGCCACAGAGCAGCCCCC- 1351	1321
È	1443	1443 AAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCACCCTGTGGCTGTAGAGGTGA 1502	1502
qq	1352	1352 AAGACCTGAGGCCGGGGAGATGATGCAAGCTCACTGACGAGCCAGTCTGCAGACGCAA 1409	1409
ò	1503	1503 CC 1504	
ΩP	1410	1410 GC 1411	
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GenCore version 5.1.7
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OM nucleic - nu	OM nucleic - nucleic search, using sw model
Run on:	March 17, 2006, 10:52:50 ; Search time 580 Seconds (without alignments) 6359.928 Million cell updates/sec
Title: Perfect score: Sequence:	US-10-649-193-14 re: 1582 l cgadccdaacacaccaccactctcccctacaaccata 1582

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

Total number of hits satisfying chosen parameters: 8023312 seqs, 1165852854 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Published Applications NA New:\*

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13: /cgn2\_6/ptodata/1/pubpna/USII\_NEW\_PUB.seq:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		æ				
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1019.2	~	64.4	2044	12	US-11-136-527-2840	Sequence 2840, Ap
ш,	545	34.5	1626	12	US-11-136-527-2713	Sequence 2713, Ap
464	7	29.3	9	12	US-11-136-527-6936	Sequence 6936, Ap
286	7.5	18.1	9	12	US-11-136-527-6809	Sequence 6809, Ap
14	8.	9.5	1400	12	US-11-136-527-6986	Sequence 6986, Ap
14	4.8	9.5	1815	12	US-11-136-527-2890	Sequence 2890, Ap
13	4.2	8.5	5192	12	US-11-136-527-2085	Sequence 2085, Ap
12	9.6	8.2	3066	12	US-11-136-527-3765	3765,
12	128.4	8.1	3453	12	US-11-136-527-1893	
H	4.6	7.9	3434	12	US-11-136-527-1894	
	124	7.8	613	9	US-09-925-065A-506766	•
12	120.2	7.6	1806	12	US-11-136-527-4065	Sequence 4065, Ap
7	115.4	7.3	2065	12	US-11-136-527-2547	Sequence 2547, Ap
	98	6.2	2786	12	US-11-128-061-870	Sequence 870, App
	98	6.2	2786	12	US-11-128-049-870	Sequence 870, App
o,	7.7	5.8	2715	12	US-11-136-527-2099	Sequence 2099, Ap
o	90.4	5.7	2121	12	US-11-136-527-3511	Sequence 3511, Ap
	90	5.7	1977	12	US-11-136-527-2881	Sequence 2881, Ap
7	9.5	5.0	1640	σ	US-11-245-147-163	Sequence 163, App
_	9.5	5.0	1640	12	US-11-090-439-30	Sequence 30, Appl

Sequence 28, Appl	Sequence 2605, Ap	Sequence 312, App	Sequence 175, App	Sequence 6, Appli	Sequence 2148, Ap	Sequence 56927, A	Seguence 56927, A	Sequence 2392, Ap	Seguence 3528, Ap	Seguence 3510, Ap	Sequence 3512, Ap	Sequence 931911,	Seguence 951357,	Sequence 931299,	Sequence 951064,		Sequence 7624, Ap		Sequence 506765,	Sequence 506762,	Sequence 506763,	Sequence 506764,	Sequence 8161, Ap	
US-11-090-439-28	US-11-030-433-27	US-10-821-234-312	US-11-245-147-175	US-11-127-877-6	US-11-136-527-2148	US-10-750-185-56927	_	US-11-136-527-2392		US-11-136-527-3510	US-11-136-527-3512	US-09-925-065A-931911	US-09-925-065A-951357	US-09-925-065A-931299	US-09-925-065A-951064	US-11-136-527-7606		US-11-136-527-6977	US-09-925-065A-506765	US-09-925-065A-506762	US-09-925-065A-506763	US-09-925-065A-506764	US-11-136-527-8161	
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### ALIGNMENTS

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Sequence 2840, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVERTION: Probe Arrays For Expression Profiling of Rat Genes

TITLE OF INVERTION PROBE ARRAYS FOR EXPRESSION PROFILING DATE: 2005-05-1010086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT PLING DATE: 2005-05-25

FRIOR APPLICATION NUMBER: US 60/574,294

PRIOR APPLICATION NUMBER: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 2044
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OTHER INFORMATION: n is a, c, g,
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OTHER INFORMATION: n is a, c, g,
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LOCATION: (60)—(60)
OTHER INFORMATION: n is a, c, g
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LOCATION: (217)..(217)
OTHER INFORMATION: n is a, o
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NAME/KEY: misc feature
LOCATION: (77) ... (77)
OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
LOCATION: (63)...(65)
OTHER INFORMATION: n is a,
JS-11-136-527-2840
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Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 03186-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362810
SOFTWARE: Patentin version 3.2
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                                                                  | FEATURE:
| NAME/KEY: misc feature
| LOCATION: (500)...(501)
| OTHER INFORMATION: n is a, c, g, or
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| NAME/KEY: misc feature
| LOCATION: (535)...(540)
| OTHER INFORMATION: n is a, c, g, or
| US-11-136-527-2840
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LOCATION: (341)...(342)
OTHER INFORMATION: n is a,
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Query Match 29.3%;
Best Local Similarity 87.4%;
Matches 527; Conservative 1
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US-11-136-527-6936
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Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wyeth

TITLE OF INVENTION Probe Arrays For Expression Profiling of Rat Genes

FILE OF INVENTION PROBE 041000 (AM101086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

FRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

LENGTH: 600
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APPLICANT: Worth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-05
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NOS 6809
LENGTH: 600
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Sequence 6986, Application US/11136527

Publication No. US20650287570A1

GRNERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Mounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
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Pred. No. 2.2e-62;
0; Mismatches 88;
                                                                                                                                                                                                                                                                                      Sequence 6809, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Local Similarity 79.4%;
Matches 339; Conservative
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US-11-136-527-6809
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                                                                                                                                                                                                                                                                                                                                                                                        Score 144.8; DB 12; Length 1400;
Pred. No. 1e-26;
1; Mismatches 353; Indels 30;
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; FILE REFERENCE: 031896-041000 (AM101086); CURRENT APPLICATION NUMBER: US/11/136,527; CURRENT FILING DATE: 2005-05-25; PRIOR APPLICATION NUMBER: US 60/574,294; PRIOR FILING DATE: 2005-05-26; NUMBER OF SEQ ID NOS: 362830; SOFTWARE: PatentIn version 3.2; SEQ ID NO 6986; LENGTH: 1400
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 52.6%;
Matches 426; Conservative
                                                                                                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Rattus norvegicus US-11-136-527-6986
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1304 ACCGGTGGCAGGACAAGCACTCGATGCCGTGCCCGAGTGGCCCGTGCCATGTCCATGCCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/5774,294
PRIOR PILING DATE: 2005-05-26
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                                                                                                                                           1364 CCTCCCCAACCCGTGTCAGCTTTCACAGCA 1393
                                                                                                                                                                                                            1483 ACGCCACCAACGCCCCCACCCACCACCA 1512
                                                                                                                                                                                                                                                                                                                     RESULT 7
US-11-136-527-2085
US-11-136-527-2085
Sequence 2085, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
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US-11-136-527-2085
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LENGTH: 5192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            895 CCAACTACGCATGGCTGYTGGTGGAGGCCTCTACCTTCACACTCCTTCGCCATCTCCT
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                                                        Sequence 2890, Application US/11136527

Reduction No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat General Reference: 031896-041000 (AMI01086)

CURRENT APPLICATION NUMBER: US/11/136,527

CURRENT FILING DATE: 2005-05-25

PRIOR PILING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2
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Pred. No. 1.1e-26;
1; Mismatches 353; Indels
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Best Local Similarity 52.6%;
Matches 426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-2890
                              US-11-136-527-2890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2890
LENGTH: 1815
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                                                                                                                                                                                                                    TTGTCAACAATGAGGTCCAGATGGAGTTTCGGAAGAGCTGGGAGCGCTGGAGGCTGGAGC 1286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1227 -----GAGTACGGAGACCCACTTGCTTTACATCCATGGACCCGTCATGGGGGGCTCTG 1281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCCTCCTGGGCATCACCTACATGCTGTTCTTCGTCAATCCCGGGGAGGATGAGGTCTCC 1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCCCTGCTGGGGATCCAGTTTGTGTGTTTCCCTGGAGGCCCTCCAACAAAGTGCT---T 1458
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                                                                                                                                TOCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAGC
                                                                                                                                                                                                                                                                                                   1322 ACTCGATCCGTGCCCGAGTGGCCCGTGCCATGTCCATCCCCACCTCCCCAACCCGTGTCA
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APPLICANT: Wyeth
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031895-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
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Publication No. US20050287570A1
GENERAL INFORMATION:
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Matches 323; Conservative
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                                                                                                                                                                                                                                                       1243 GTGTCTGTGTTCTACTGTTTCCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGG 1302
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TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 031896-041000 (AM101086)
CURRENT APPLICATION NUMBER: US,11/136,527
CURRENT FILING DATE: 2005-05-25
FRIOR APPLICATION UNMER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 3765
LENGTH: 3066
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Pred. No. 8.2e-23;
0; Mismatches 309;
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Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Lodal Similarity 52.0%;
Matches 344; Conservative (
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APPLICANT: Mount
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7.8%; Score 124; DB 6; illarity 100.0%; Pred. No. 1.5e-21; Conservative 0; Mismatches 0;
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; Sequence 506766, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: PatentIn version 3.2
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US-09-925-065A-506766
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Best Local Similarity
Matches 124; Conserv
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LENGTH: 1806
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                                                                                                                                          1519 ACTATCTACTGCTTCTGTAACCATGAGGTGCAAGTGACCCTGAAGCGTCAGTGGGCGCAG 1578
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REPERENCE: 031896-041000 (AMI01086)
CURRENT APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US/11/136,527
PRIOR PELING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SEQ ID NO 1894
LENGTH: 3434
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Pred. No. 1.5e-21;
0; Mismatches 269;
                                                                                                                                                                                                                                                                                                                                                      Sequence 1894, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
APPLICANT: Wyeth
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Best Local Similarity 53.1%;
Matches 315; Conservative 0
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US-11-136-527-1894
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Publication No. US20050287570A1
SEGRERAL INFORMATION:
APPLICANT: Worth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes FILE REFERENCE: 03186-041000 (AM101086)
CURRENT FILING DATE: 2005-05-25
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR PILING DATE: 2000-11-16
PRIOR PILING DATE: 2000-11-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-01-16
PRIOR PELING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 506766
LENGTH: 613
1268 ATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320
                                                          1480 Accargaderecanderenciereandeerencadeerecanderecandeerecand 1532
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NAME/KEY: misc feature
LOCATION: (132)...(151)
OTHER INFORMATION: n is a,
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US-11-128-061-870
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Publication No. US20050287570A1

GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Wounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031896-041000 (AM101086)
CURRENT FILING DATE: 2005-05-25
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR PILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Percentin version 3.2

SEG ID NO 2547
LENGTH: 2065
                                                                                                                                                                                                                                                                                                                                            866 GCATTGGCTGGGGTGTGCCCTTCCCCATTGTGGGCCTGGGCCATTGGGAAGCTGTACT
                                                                                      686 AGCTAACCATGAGCCCCGAGGTCCACAGAGCAACGTGGGCTGGTGCAGGTTGGTGACAG
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  7.6%; Score 120.2; DB 12; Length 1806; 2.6%; Pred. No. 1.7e-20; ve 0; Mismatches 293; Indels 9;
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Pred. No. 2.9e-19;
9; Mismatches 255; Indels
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Best Local Similarity 52.4%;
Matches 314; Conservative
Query Match 7.6%;
Best Local Similarity 52.6%;
Matches 335; Conservative
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GGTGCAGGTTGGTGACAGCCGCCTACAACTACTTCCATGTGACCAACTTCTTCTGGATGT
                              TCGGCGAGGGCTGCTACCTGCACACACCATCGTGCTCACCTACTCCACTGACCGGCTGC
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SOFTWARE: Patentin version 3.3
SEQ ID NO 870
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ORGANISM: Cricetulus
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1176 CACGCTGACGCTGGTGCCCCTGCTGGGTGTCCACGAGGTGGTGTTTGCCCCCGTGACGGA 1235
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Pred. No. 7.3e-15;
0; Mismatches 265; Indels
; FILE REFERENCE: 01997.027700
; CURRENT APPLICATION NUMBER: US/11/128,049
; CURRENT FILID DATE: 2005-05-11
; PRIOR APPLICATION NUMBER: US 60/570,425
; PRIOR FILING DATE: 2004-05-11
; NUMBER OF SEQ ID NOS: 7285
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 870
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Publication No. US20060010513A1
GENERAL INFORMATION:
APPLICANT: Melville, Mark W.
APPLICANT: Melville, Milliam M.
APPLICANT: Hann, Louene E.
APPLICANT: Hann, Louene E.
APPLICANT: Leonard, Mark W.
APPLICANT: Leonard, Mark W.
APPLICANT: Leonard, Mark W.
APPLICANT: Leonard, Mark W.
APPLICANT: Miller, Christopher P.
TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR
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; NAME/KEY: misc_feature
; LOCATION: (1560)..(1607)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (2217)..(2276)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (2561)..(2580)
; OTHER INFORMATION: n is a, c, g, or t
US-11-128-061-870
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US-11-128-049-870
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Search completed: March 17, 2006, 11:08:49 Job time : 583 secs

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Mouse Mouse Mouse Rat

Abg76401 N Adj65808 N Ado29266 N Ado50803 n Aar69521 N

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Rat

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Aao19427 B Aao19439 B Abu08077 B

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Abg76048 Ade62732 Adj65801 Ado50797 Ado50821

Human CRH cort

Aau96998

AAU96998 ADO5082

ALIGNMENTS

Run on:

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Human; CRF1; corticotropin releasing factor receptor 1; h15571; immunomodulatory; vascular; hepatic; antiasthma; anitmicrobial; antiinflammatory; immunosuppressive; gene therapy; vaccine; G-protein coupled receptor; GFK; liver fibrosis; respiratory disorder; infection; chronic inflammatory disease; organ-specific autoimmunity; graft rejection; cystic fibrosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding a G-prot. coupled receptor polypeptides, useful for preventing, diagnosing and treating, e.g. liver fibrosis and asthma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is a human G-protein coupled receptor (GPCR) used for comparison with the seven transmembrane domain of a novel GPCR designated h15571. h15571 GPCR polynucleotides and polypeptides may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate GPCR expression. Such diseases includes immune, haematological, fibrotic, hepatic and respiratory disorders including asthma, allergies (e.g. allergic rhinitis and psoriasis), pathogenic infections, chronic inflammatory diseases, organ-specific autoimmunity,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human CRF1 seven transmembrane domain.
                                                                                    ADJ65808
ADO29266
ADO29266
AR69521
AR69523
ABU62361
AR019427
AR019437
AR019437
AR019437
ABU6077
ABG76048
ABG76048
ABG76048
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29-FEB-2000; 2000US-00515781.
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WO200109328-A1.
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Human CRF
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Non-endog
Mouse CRF
                                                                                                                       March 16, 2006, 17:12:55 ; Search time 192 Seconds (without alignments) 1016.063 Million cell updates/sec
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                                                                                                                                                                                                                                  1 MGGHPQLRLVKALLLLGLNP......SIPTSPTRVSFHSIKQSTAV 444
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                    GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                        2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                                        protein search, using sw model
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ABG76402
ADE62734
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AAR97290
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AAE26679
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geneseqp2003bs:*
geneseqp2004s:*
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geneseqp2000s:*
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geneseqp2002s:*
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2381
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Similarity
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07-JUN-1995;
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Best Local S
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graft rejection, graft versus host disease, cystic fibrosis and, in particular, liver fibrosis. The GPCR polypeptides may be used as antigens in the production of antibodies against GPCR and in assays to identify modulators (agonists and antagonists) of GPCR expression and activity. The anti-GPCR antibodies and GPCR attagonists may also be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used to down regulate GPCR expression and activity. The anti-GPCR antibodies may be used as diagnostic agents for detecting the presence of GPCR polypeptides
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                                                                                                                                                                                       1 MGGHPQLRLVKALLLIGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, G protein-coupled corticotropin-releasing factor receptor; CRF;
                                                                                                                                                                                                                                                                121 IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
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                                                                                                                             444;
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93US-00110286
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ID AAE26685 standard; protein;
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                                                                                                                                                 Matches 444; Conservative
                                                                                                                                       Local Similarity
                                                                                                      Sequence 444 AA;
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23-AUG-1993;
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The invention relates to recombinant mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having high affinity for CRF and nucleic acid molecules encoding such receptor proteins. Polypeptides of the invention can be used to reduce high levels of adrenocorticotrophic hormone caused by excess CRF and so can be used to treat diseases such as Cushing's syndrome, pituitary tumours, chronic stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They are used in pharmaceuticals and in the production of antibodies. The present sequence is human CRF-RA2 splice variant protein
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94WO-US005908.
94US-00353537.
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VALE W W.
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SAWCHENKO P.
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N-PSDB; AAD44489.
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Novel DNA encoding corticotropin releasing hormone receptor type 1 which is useful for treating pathophysiological state such as inflammatory skin disease e.g. psoriasis and allergic contact dermatitis.
                                                                                          Human; corticotropin releasing hormone receptor type 1; CRH-R1; antipsoriatic; antiallergic; immunosuppressive; antinflammatory; dermatological; pathophysiological state; neuroendocrine disorder; hyperproliferative epidermal disorder; allergic contact dermatitis; autoimmune disorder; epidermal carcinogenesis; malignant transformation; epidermal melanocyte; chromosome 17.
                                                                        Human CRH-R1 beta protein SEQ ID NO:2.
                                                                                                                                                                                                                                                                                                                                                                                      Example 5; Fig 5A-C; 110pp; English.
         ABR43052 standard; protein; 444 AA.
                                                                                                                                                                                                                                                                              (UYTE-) UNIV TENNESSEE RES CORP.
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                                                  (first entry)
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                                                                                                                                                                       Homo sapiens.
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                                                  03-JUL-2003
                                                                                                                                                                                                                27-MAR-2003
                               ABR43052;
ABR43052
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The present invention describes DNA (I) encoding a corticotropin releasing hormone receptor type 1 (CRH-R1) protein comprising an amino acid sequence given in ABR43055 to ABR4301. Also describe: (I) a vector (II) capable of expressing (I) or its degenerate variant, and comprising (I) or its degenerate variant, and regulatory elements necessary for expression of the DNA in a cell; (2) a host cell (III) transfected with (IV) directed against (IV); (5) a host cell (III) transfected with (II); (3) an isolated CRH-R1 protein (IV) encoded by (I); (4) an antibody (V) directed against (IV); (5) a paramaceutical composition (VI) comprising (IV), and a carrier; and (6) protecting (M) skin cells against campage induced by an environmental factor, by inducing the expression of CRH-R type IG in the skin cells, where the expression of the receptor protects the skin cells against the damage. CRH-R1 has antipsoriatic, antiallergic, immunosuppressive, antiinflammatory and dermaclological cativities. (VI) can be used for treating a pathophysiological state such as hyperproliferative epidermal disorder, neuroendocrine disorder, allergic context dermallergic autoimmuntal factor such as solar radiation. Human CRH-R1 call allergic and environmental factor such as solar radiation. Human CRH-R1 is located to chromosome context such as solar radiation. Human CRH-R1 is located to chromosome context in the present sequence represents human CRH-R1 beta (see Genbank context) in the present sequence represents human CRH-R1 beta (see Genbank context) in the context of th

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100.0%; Score 2381; DB 6;
100.0%; Pred. No. 8.9e-245;
iive 0; Mismatches 0;
                    Best Local Similarity 100.
Matches 444; Conservative
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Length 444;

Query Match

61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120

1 MGGHPQLRLVKALLLIGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA

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ABU08081 standard; protein; 444 AA. RESULT 4 ABU08081

(first entry) 21-MAY-2003 ABU08081;

G protein-coupled corticotropin-releasing factor receptor;
hypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH;
adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease;
Cushing's disease; anorexia nervosa; alcoholism; antiinflammatory;
irritable bowel syndrome; melancholic depression; neuroprotective;
nootropic; antidepressant; splice variant. Human; receptor; corticotropin-releasing factor receptor; CRF; Human corticotropin-releasing factor receptor 2 (CRF-R2).

Homo sapiens

95US-00374009 17-JAN-1995; US6495343-B1 17-DEC-2002 

vale WW, (SALK ) SALK INST BIOLOGICAL STUDIES. Chen R, Lewis KA, WPI; 2003-327461/31. Perrin MH,

N-PSDB; ABX93041.

93US-00079320. 93US-00110286. 94WO-US005908.

94US-00353537

25-MAY-1994;

18-JUN-1993; 23-AUG-1993; P,

Sawchenko

Donaldson CJ,

New nucleic acid and its encoded G protein-coupled corticotropin-releasing factor receptor, useful for diagnosing or treating e.g. ACTH levels or high cortisol levels associated with Alzheimer's disease or Cushing's disease

Disclosure, Col 61-64; 42pp; English.

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                mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein. CRF is a hypothalamic peptide which stimulates the screetion and biosynthesis of pituitary adrenociticotrophic homone (ACTH) leading to increased adrenal glucocorticotrophic homone (ACTH) leading to receptor that it encodes, is useful in bioassays. The nucleic acid or CRF receptor is particularly useful for providing recombinant receptors that allows the development of less expensive, more sensitive and automated means for assaying CRF and CRF-like compounds and developing CRF-based useful in therapy, e.g. gene therapy for reducing ACTH levels or treating high cortisol levels associated with Alzheimer's diseases, Cushing's
                                                                                                                                                                                                                                                                  diseases, anorexia nervosa, alcoholism or irritable bowel syndrome. These tase useful in diagnostic assays, e.g. for diagnosting Alzhaimer's diseases, melancholic depression, anorexia nervosa, Cushing's diseases or alcoholism. The sequence presented is the human splice variant of CRF-R1,
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  The invention discloses an isolated nucleic acid, which encodes a
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Novel cell line expressing nucleic acid expression vector comprising nucleic acid encoding human corticotropin releasing factor (CRF) receptor useful for reducing high adrenocorticotropin hormone, by binding to CRF.

Disclosure; Col 61-64; 42pp; English.

Sawchenko P;

Donaldson CJ,

Chen R, Lewis KA, Vale WW,

WPI; 2003-287359/28

Perrin MH,

N-PSDB; ABX11840

SALK ) SALK INST BIOLOGICAL STUDIES.

95US-00483139.

07-JUN-1995;

17-JAN-1995

93US-00079320. 93US-00110286. 94WO-US005908. 94US-00353537. 95US-00374009.

25-MAY-1994; 09-DEC-1994;

18-JUN-1993

23-AUG-1993

26-MAY-2000; 2000US-00580734.

19-NOV-2002

Homo sapiens. US6482608-B1

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receptor in a suitable host cell, by expressing a recombinant CRF receptor in a suitable host cell, by expressing a recombinant CRF receptor in a suitable host cell, by expressing the vector, where the receptor in a suitable host cell, by expressing the vector, where the nucleic acid encodes CRF-R that binds CRF or nucleic acid degenerate to the naturally occurring nucleic acid. The cell line is useful for expressing hCRF-RAI protein by recombinant techniques and in binding cassays using CRF-R which are used for rapidly screening large number of compounds to determine which compounds are capable of binding to CRF-R, and for identifying new CRF-like ligands. The polypeptides expressed by the call line inhibit CRF-like ligands. The polypeptides expressed by care useful for reducing high ACTH) release in vitro by several cells, and adrenocorticotropin hormone (ACTH) release in vitro by several cells, and case useful for reducing high ACTH levels caused by excess CRF, and can elacted the proteins are also useful for treating cushing's disease, pituitary tumours, Alzheimer's disease, melancholic depression, anorexia nervosa, chronic stress, alcoholism and hypercortisolaemia. The proteins are also useful for treating such as pre-eclampsia, which occur during pregnancy, to reduce pregnancy-induced complications and increased CRF levels which can otherwise result in excessive release of ACTH. The proteins are also useful for locally treating arthritis and other similar aliments, modulating action of CRF in mammals. The CRF-R polypeptides are used in such as as the diagnosis and/or treatment of CRF-dependent tumours, chancing the survival of brain neurons, inducing abortion in livestock and other domesticated animals, inducing twinning in livestock and other homesticated animals, inducing the proteins are applied to the contraction of CRF in mammals, inducing abortion in livestock and other domesticated animals, inducing the proteins are applied to the contraction of the factor of the factor of the factor of the factor 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a cell line expressing a recombinant corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid expression vector, or a cell line containing a nucleic acid vector encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A,
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100.0%; Pred. No. 8.9e-245;
ive 0; Mismatches 0;
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Human; receptor; corticotropin releasing factor receptor; hCRF-RAl; Cushing's disease; pituitary tumour; Alzheimer's disease; melancholic depression; anorexia nervosa; chronic stress; alcoholism; hypercortisolaemia; gastrointestinal disorder; irritable bowel syndrome; pre-eclampsia; pregnancy-induced complication; arthritis; abortion;

twinning

ABG76402 standard; protein; 444 AA

RESULT 5 ABG76402 Human hCRF-RA1, splice variant.

(first entry)

07-MAY-2003 ABG76402;

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                                                                                                                                                                                  241 YLHTAIVLTYSTDRLRKKWFICIGWGVPFPIIVAWAIGKLYYDNBKCWFGKRPGVYTDYI 300
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61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragmen derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent
                                                                                                181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                181 NITHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
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                                                VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV
                                IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
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(FARB ) BAYER AG.
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that increases or decreases the expression of the polymucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the composition, a method for producing a pharmaceutical composition, a certod for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the compositioation, a method for identifying a compound useful in rreating pain and a pharmaceutical composition compound useful in rreating colypeptides or their antibodies. The polymucleotide or the compound that colypeptides or their antibodies. The polymucleotide or the compound that compliants its activity is useful for preparing a medicament for treating pain and expiral sequence presented is a human protein (shown in Table 2 of the rappy). The sequence presented is a human protein (shown in Table 2 of the sequence data for this patent did not form part of the printed consecution) which is differentially expressed during pain. Note:

The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at the way of the printed consecution in the patent did not form part of the printed specification.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 2381; DB 7; Length 444; 100.0%; Pred. No. 8.9e-245; ive 0; Mismatches 0; Indels 0
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Matches 433; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein or polypeptide from Rat, Mouse or human appearing as AD055801, AD055805, or AD055810, encoded by the nucleic acids appearing as AD058800, AD055802, AD055810, encoded by the nucleic acids appearing as AD058800, AD058802, AD055810, encoded by the nucleic acids appearing as AD058800, AD058802, AD058804, or AD058809. Also included are a composition comprising CRF-R, assaying C for the presence in biological fluids of CRF-R protein, protein analogues and/or fragments, comprising CRF-R) and/or one or more antibodies. The protein, polynucleotide or composition is useful in diagnosing and c treating Alzheimer's disease, melancholic depression, anorexia nervosa, Cushing's disease, hypercortisolaemia or alcoholism, gastrointestinal disorders (e.g. irritable bowel syndrome) or physiological conditions and in modulating blood pressure, thus combat hypotension. The present sequence represents human splice variant CRF-RA2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 YLHTAIVLTYSTDRLRKWMPICIGWGVPPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECOBILNEBKKSKVHYHVAV 120
                                                                                                                                                                                                                                                                                                                                     New mammalian G protein-coupled corticotropin-releasing factor receptor protein, useful in diagnosing and treating Alzheimer's disease, anorexia nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIIHWNLISAFILRNATWFVVQLTMSPEVHOSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                       Sawchenko
gastrointestinal disorder; irritable bowel syndrome; inflammation;
Addison's disease; cardiac perfusion; blood pressure; hypotension.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 2381; DB 8; Length 444; 100.0%; Pred. No. 8.9e-245; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                       Donaldson CJ,
                                                                                                                                                                                                                                                                      Vale WW,
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7; SEQ ID NO 15; 44pp; English.
                                                                                                                                                                                                                                          (SALK ) SALK INST BIOLOGICAL STUDIES
                                                                                                                                                                                                                                                                      Chen R, Lewis KA,
                                                                                                                                              93US-00079320.
93US-00110286.
94WO-US005908.
94US-00353537.
95US-00483139.
                                                                                                                                                                                                                98US-00191724.
                                                                                                                      2003US-00649193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 444, Conservative
                                                                                                                                                                                                                                                                                               WPI; 2004-203293/19.
N-PSDB; ADJ65809.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 444 AA;
                                                                US2004039173-A1
                                                                                                                      26-AUG-2003;
                                         Homo sapiens
                                                                                                                                                                                                                12-NOV-1998;
                                                                                                                                                                                      09-DEC-1994;
                                                                                                                                                                           25-MAY-1994
                                                                                                                                                 18-JUN-1993
                                                                                                                                                                                                      07-JUN-1995
                                                                                                                                                                                                                                                                      Perrin MH,
                                                                                                                                                                                                                                                                                                                                                                                hypotension
                                                                                          26-FEB-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide, useful for preparing a composition for treating a patient in need of increased or suppressed activity or expression of the guanosine triphosphate-binding protein coupled receptor.
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301 YQGPMILVILINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPILGITYMLFF
                                                                                        VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11 KALLLIGINPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; GPCR; guanosine triphosphate-binding protein coupled receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
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Pred. No. 1.1e-238;
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                                                                                                                                                                                                                   421 ARAMSIPTSPTRVSFHSIKQSTAV 444
                                                                                                                                                                                                                                                            421 ARAMSIPTSPTRVSFHSIKQSTAV 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human GPCR protein SEQ ID NO:708
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADC86255 standard; protein; 447
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Claim 3; Page 65; 84pp; English.
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93US-00110286
                                       Lewis
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                                                                                                                                                                                                                                                          Best Local Similarity 93.5
Matches 415; Conservative
                                     Chen R,
                                                        WPI; 1995-052077/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                        Local Similarity
                                                                 N-PSDB; AAQ81952
                                                                                                                                                                                                                             Sequence 415 AA;
23-AUG-1993;
                                                                                                     pituitary tu
antagonists.
                                      Perrin MH,
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                                             194 FILRNATWFVVQLTMSPEVHQSNVGWCRLVTAANNYFHVTNFFWMFGBGCYLHTAIVLTY
                                                                                       STDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVTDYIYQGPMILVLL
                                                                                                                311 INFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSR
                                                                                                                           314 INPIFIFINIVRILMIKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFVNPGEDEVSR
                                                                                                                                                    VVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARVARAMSIPTSP
                                                                                                                                                               374 VVPIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARVARAMSIPTSP
                                                                           STDRLRKWMFICIGWGVPFFIIVAWAIGKLYYDNBKCWFGKRPGVYTDYIYQGPMILVLL
                                       PILRNATWPVVOLTMSPBVHOSNVGWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTY
                                                                                                                                                                                                                                                                                                                                           Pituitary; hormone; corticotropin releasing factor receptor; hypothalamus; adenocorticotrophic hormone; ACTH; Cushing's disease; pituitary tumor; diagnosis.
                                                                                                                                                                                                                                                                                                                           Hùman pituitary corticotropin releasing factor receptor CRF-RA1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "protein-kinase-C phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "protein-kinase-C phosphorylation site"
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                                                                                                                                                                                        TRVSFHSIKQSTAV 444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated corticotropin releasing factor receptor and nucleic acid - also antibodies, useful for diagnosis and treatment of Cushing's disease, pituitary tumours etc., also to identify specific agonists and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                             This protein can be used to determine CRF (e.g. over- or under-
production, high levels of CRF late in pregancy may indicate trisk of
premature labor). Cells expressing the protein are used to identify e.g.
antibodies, which can be used to modulate signal transduction activity
mediated by CRF receptors. Typical applications are in the treatment of
Cushing's disease, pituitary tumors, etc. (Updated on 25-MAR-2003 to
correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 YLHTAIVLTYSTDRLRKMMFICIGMGVPFPIIVAWAIGKLYYDNBKCWFGKRPGVTDYI
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                                                        Donaldson CJ
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93.5%; Pred. No. 4.8e-224;
ive 0; Mismatches 0;
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(SALK ) SALK INST BIOLOGICAL STUDIES
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211 300 271

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A new G-protein-coupled receptor protein, CRF-R1 (AAR97290), has high binding affinity for corticotropin releasing factor (CRF). The amino acid agequence was deduced from a cDNA clone (AAR28968) isolated from human pituitary corticotrope adenoma (Cushing's tumour). This cDNA can be used for prodn. of recombinant CRF-R1. A splice variant contg. a 29-amino acid insert (AAR97291) was also identified. The receptor can be used to identify agonists and antagonists that modulate the signal transduction activity mediated by CRF receptors. The receptor can be administered therapeutically to reduce high ACTH levels caused by excess CRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isolated corticotropin-releasing factor receptor (CRF-R) - used to develop prods. for modulating signal transduction activity mediated by
Corticotropin releasing factor receptor; CRF-R; corticoliberin; signal transduction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= Phosphorylation site
/note= "protein kinase C phosphorylation site"
                                                                                                                                                                                                                                                                   /label= Phosphorylation site note= "protein kinase \overline{\mathbf{C}} phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                               /label= Phosphorylation site
/note= "casein kinase II phosphorylation site"
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/note= "protein kinase © phosphorylation site"
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/note= "protein kinase A phosphorylation site"
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                                                                            Location/Qualifiers
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95US-00374009
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Donaldson CJ,

Vale WW,

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This sequence represents human corticotropin releasing factor (CRF) receptor protein. The cDNA fragment is derived from the expression vector designated pACO2. pACO2 is an expression vector constructed for elevated expression of the human receptor protein. The recembinantly produced CRF receptor protein or a peptide fragment, may be used for efficient and rapid screening of an agonist or antagonist of human CRF receptor.
                                                          61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      corticotropin releasing factor; CRP; receptor; expression vector; agonist; antagonist; blood pressure; immunosuppression.
       1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                        GOLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECOEILNEEKKSKVHYHVAV
                                                                                                                                       121 IINYLGHCISLVALLVAFVLFLRL
                                                                                                                                                                                            NITHWILISAFILKNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGBGC
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                                                                                                         121 IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human corticotropin releasing factor receptor protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    392 ARAMSIPTSPTRVSFHSIKQSTAV 415
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N-PSDB; AAT37068.
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                                                                                                  MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                                                                                                                                                                      212 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI
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Agonists may be used for lowering blood pressure, and antagonists may used for the treatment of immunosuppression
                                                                                       1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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                                               91.8%; Score 2186.5; DB 2; 93.5%; Pred. No. 4.8e-224; iive 0; Mismatches 0;
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93US-00110286.
94WO-US005908.
94US-00353537.
95US-00483139.
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                                                          Best Local Similarity 93.5
Matches 415; Conservative
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                                                         Local Similarity
                             Sequence 415 AA;
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23-AUG-1993;
25-MAY-1994;
09-DEC-1994;
07-JUN-1995;
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The invention relates to recombinant mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having high affinity for CRF and nucleic acid molecules encoding such receptor proteins. Polypeptides of the invention can be used to reduce high levels of adrenocorticotrophic hormone caused by excess CRF and so can be used to treat diseases such as Cushing's syndrome, pituitary tumours, chronic stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They are used in pharmaceuticals and in the production of antibodies. The present sequence is human CRF-RAI protein
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                                                                                                                                                                                                                                                             New isolated recombinant mammalian G protein-coupled corticotropin-
releasing factor receptor protein for treating e.g. Cushing's syndrome,
pituitary tumors, stress, anorexia, alcoholism or irritable bowel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 YLHTAIVLTYSTDRLRKAMPICIGWGVPPPIIVAWAIGKLYYDNEKCWFGKRPGVTDYI
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                                                                                                                                    Sawchenko
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 415;
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                                                                                                                                    Donaldson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
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                                                                                                                                    Vale WW,
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                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 22-23; 44pp; English.
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93.5%;
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                                                                                                                                    Lewis
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LEWIS K A.
VALE W W.
DONALDSON C J.
SAWCHENKO P.
                                                                                                                                    Chen R,
                                                                                                                                                                                    WPI; 2002-462916/49
N-PSDB; AAD44482.
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Best Local Similarity
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The present invention relates to a method of identifying candidate compounds for regulating skeletal muscle mass or function, and comprises contacting a test compound with a corticotropin releasing factor-2 receptor (CRP2R) or with a cell expressing a functional CRP2R, the CRP2R and identifying the test compound binds to, or activates, the CRP2R as candidate compounds for regulating skeletal muscle mass or function. The method is useful for preparing a medicament for treating skeletal muscle atrophy or for prophylactic treatment of muscular dystrophies. The present sequence is a corticotrophin releasing factor receptor
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VNPGEDEVSKVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; rat; mouse; sheep; cow; chicken; CRFIR; CRF2R;
skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
muscular dystrophy; corticotrophin releasing factor-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying candidate compounds for regulating skeletal muscle mass treating skeletal muscle atrophy by identifying test compounds that to, or activate, the corticotropin releasing factor-2 receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                    Human corticotrophin releasing factor receptor CRFIR variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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Pred. No. 4.8e-224;
0; Mismatches 0;
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                                                                                                                                                                                                                                                      AA019421 standard; protein; 415 AA
                                                                                                          392 ARAMSIPTSPTRVSFHSIKOSTAV
                                                                              421 ARAMSIPTSPTRVSFHSIKQSTAV
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91.8%;
Best Local Similarity 93.5%;
Matches 415; Conservative (
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                              332
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                                                                                                                                                                                                      RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method of identifying candidate compounds for regulating skeletal muscle mass or function, and comprises contacting a test compound with a corticotropin releasing factor-2 receptor (CRF2R) or with a cell expressing a functional CRF2R, determining whether the test compound binds to, or activates, the CRF2R and identifying the test compounds that bind to, or activates, the CRF2R as candidate compounds for regulating skeletal muscle mass or function. The method is useful for preparing a medicament for treating skeletal muscle atrophy or for prophilactic treatment of muscular dystrophies. The present sequence is a corticotrophin releasing factor receptor
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bind
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                                                                            Human; rat; mouse; sheep; cow; chicken; CRFIR; CRF2R;
skeletal muscle atrophy; corticotrophin releasing factor-2 receptor;
muscular dystrophy; corticotrophin releasing factor-1 receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Identifying candidate compounds for regulating skeletal muscle mass treating skeletal muscle atrophy by identifying test compounds that to, or activate, the corticotropin releasing factor-2 receptor.
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                              corticotrophin releasing factor receptor CRF1R
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Matches 415; Conservative
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                                                                                                                                                                                                                                                      WO200269908-A2
                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                        gene therapy
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The invention relates to a Schizosaccharomyces pombe yeast cell (I) comprising: (a) a heterologous G-Protein Coupled Receptor (GPCR) - regulated signaling pathway (PI) which is derepressed during mitotic phase of cell growth; and (b) a reporter system (RS) for reporting signal mediated by PI, which is regulated by EQCK, and GI and PR is promoter (PR), which is regulated by GPCK, and GI and PR is heterologous. Also described is (I) an isolated polynucleotide (IIa) comprising an sxa2 promoter, or its homologue or analogue, operatively linked to an exogenous reporter gene; (2) an isolated polynucleotide (IIb) encoding a Galpha-transplant having a nucleotide sequence from Galphaq, Galphae, Galphai2, Galphai3, Galphaz, Galphai2,
                                                                                                                                                                                                               New Schizosaccharomyces pombe cell, useful for studying G-protein coupled receptor-regulated signaling pathway that is derepressed during cell growth mitotic phase and
                              240
                                                             211
                                                                                        300
                                                                                                                      271
                                                                                                                                                     YQGPMILVLLINFIFLFNIVRILMTKLRASTTSBTIQYRKAVKATLVLLPLLGITYMLFF 360
                                                                                                                                                                                   331
----RSIRCLR 151
                                                                                                           YLHTAIVLTYSTDRLRKWMPICIGWGVPPPIIVAWAIGKLYYDNBKCWFGKRPGVYTDYI
                                                                                                                                                                          YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF
                                            YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI
                              NI IHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yeast, G-Protein Coupled Receptor, GPCR-regulated signaling pathway, GPCR; sxa2 promoter, Galpha-transplant, Galphaq, Galphas, Galphao, Galphai2, Galphai2, Galphai2, Galphai2, Galphai6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Page 85-87; 117pp, English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human corticotrophin releasing hormone.
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IINYLGHCISLVALLVAFVLFLRL-
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Galphal3, Galphal4 and Galphal6. (I), (IIa) or (IIb) is useful for studying GPCR-regulated activity, for determining the effect of a compound on GPCR-regulated activity by introducing the compound, to (I) and noting the output of RS, where the compound affects the ability of orphan GPCR to regulate RS. Furthermore (I) is useful for identifying a reagent that modilates GPCR-regulated pathway and for identifying a reagent that modilates GPCR-regulated signaling pathways, by producing a random peptide within (I) and measuring an amount of reporter activity produced. ABRS5570-ABRS95608 represent Galphatransplant amino acid sequences and related amino acid sequences of the
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glucagon receptor	glucagon receptor glucagon-like pept	calcitonin-like re	calcitonin recepto	pituitary adenylat	pituitary adenylat	glucagon-like pept	vasoactive intesti	pituitary adenylat	growth hormone-rel	glucose-dependent	somatoliberin rece	pituitary adenylat	pituitary adenylyl	gastric inhibitory
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## ALIGNMENTS

	RESULT 1 A48260	
	Corticoliberin N;Alternate nam	corticoliberin receptor, long splice form - human Alternate names: corticoliberin binding protein; corticotropin releasing factor receptor
	C;Species: nom C;Date: 31-May- C:Accession: I6	.j.ppcres: nomo baptens (man) C.bate: 31-May-1996 #sequence_revision 11-Apr-1997 #text_change 09-Jul-2004 C.Accession: 160975: A48260: 839534
	R; Chen, R; Lev	M.B. K.A.; Perrin, M.H.; Vale, W.W. ad. Sci. U.S.A. 90, 8967-8971, 1993
	A; Title: Expres	A,Title: Expression cloning of a human Corticotropin-releasing factor (CRF) receptor. A,Reference number: A48260, MUID:94022296; PMID:7692441
	A;Accession: 160975 A;Status: translate	A;Accession: 160975 A;Status: translated from GB/EMBL/DDBJ
	A; Molecule type: mRNA A: Regidues: 1-444 < RRS>	e: mRNA 444 < RRS >
	A;Cross-referer	A.Cross-references: UNIPROT: P34998; UNIPARC: UPI0000128429; GB:L23333; NID:g408691; PIDN: A. Brossinger and A. Brossing
	A; Accession: A48260	48260
	A;Status: preliminary A:Molecule type: mRNA	A;Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: mRNA
	A, Residues: 1-1	A)Residues: 1-145,175-444 <re2></re2>
	A; Cross_referen	A;Cross_references: UNIPARC:UP1000002A/1D; GB:L23332; NID:9408689; FIDN:AAA35/18.1; FID:5 Rrvita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; Ca
-	FEBS Lett. 335,	FEBS Lett. 335, 1-5, 1993 Armifle: Primary structure and functional expression of mouse bituitary and human brain of
	A; Reference num	nber: S39534; MUID:94063063; PMID:8243652
	A;Accession: 539534 A;Status: preliminary	39534 Iminary
	A; Molecule type: mRNA A; Residnes: 1-145,175	A:Molecule type: mRNA A:Regidner: 1-145,175-444 <vit></vit>
	A,Cross-referer	
	A;Note: the sec	A;Note: the sequence from Mig. 1 is inconsistent with that from Mig. 3 in having an addit C:Genetics:
	A;Gene: GDB:CR	
	A;Cross-relerences: GDB:2355 A;Map position: 17q12-17q22	A;Cross-reierences: GUB:135922; UMIM:122561 A;Map position: 17q12-17q22
	C;Superfamily: C;Keywords: alt	C;Superfamily: glucagon receptor C;Keywords: alternative splicing; transmembrane protein
	Query Match	100.0%;
	вевт Local Similarity Matches 444; Conser	lmijarity 100.0%; Fred. No. 4.56-125; ; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
	0y 1 N	1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
-	Db 1	1 MCGHPQLRLVKALLLIGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60
	Oy 61 G	61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
	DP Q0	61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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Corticotropin releasing hormone receptor variant - human Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Cispecies: Homo sapiens (man)
Ciscession: 138879
Ciscession: 138879
Ciscession: 138879
Ciscession: 138879
Airle: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, thireference number: 138879
Airle: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, thireference number: 138879
Airle: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, thireference number: 138879
Airle: A variant of the human corticotropin-releasing factor (CRF) receptor: cloning, thireference number: 138879
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A;Molecule type: mRNA
A;Rosidues: 1-415 <RBS>
A;Rosidues: 1-415 <RBS>
A;Cross-references: UNIPROT:P35353; UNIPARC:UP1000002EF2A; GB:L25438; NID:g450298; PIDN:J
C;Superfamily: glucagon receptor
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       332 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWRRWQDKHSIRARV 391
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Pred. No. 5.6e-177;
5; Mismatches 7; Indels 29;
                                                                                                                                                                                                                                                                                                            corticotropin-releasing factor receptor - rat
C,Species: Rattus norvegicus (Norway rat)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change
C;Accession: 158144
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richang, C.P.; Pearse, R.V.; O'Connell, S.; Rosenfeld, M.G.
Neuron 11, 1187-1185, 1993
A;Title: Identification of a seven transmembrane helix receptor
A;Reference number: I58144, MUID:9409969; PMID:8274282
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                                                                                                                  ARAMSIPTSPTRVSFHSIKQSTAV
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Best Local Similarity 90.8%;
Matches 403; Conservative
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CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiSpecies: Mus musculus (house mouse)
CiDate: O'Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
CiAccession: 839535
Rivita, N.; Laurent, P.; Lefort, S.; Chalon, P.; Lelias, J.M.; Kaghad, M.; le Fur, G.; CRYITIE: Primary structure and functional expression of mouse pituitary and human brain A,Reference number: 839534; MUID:94063063; PMID:8243652
A,Accession: 839535
A,Accession: 839535
A,Accession: S39535
A,Accession: S39535
A,Accession: S39535
A,Accession: S39535
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A,Accession: S39537
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172 YQGPMILVLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLAGITYMLFF 331
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                                                                                                                                                                       181 NITHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNPFWMFGEGC
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301 YQGPMILVLLINFIFLFNIVRILMTKLRASTISETIQYRKAVKATLVLLPLLGITYMLFF
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89.8%; Score 2137.5; DB 2;
Best Local Similarity 91.2%; Pred. No. 6.2e-178;
Matches 405; Conservative 4; Mismatches 6;
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A;Molecule type: mRNA A;Residues: 1-375 <res> A;Crose-references: UNIPROT:P34998; UNIPARC:UPI000002A71E; EMBL:U16273; NID:g606973; PIL</res>	Qy 118 VAVIINYLGHCISLVALLVAFVLFIRIRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIR 177 
ngth 375;	Qy 178 CLRNIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTNPFWMFG 237 
OY 1 MGGHPQLRLVKALLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA 60	238 EGCYLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYT 
GY 61 GQLVVRPCPAPFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120	298 DYIYQGPMILVILINFIE-FNIVRILMTKRASTTSETIQYRKAVKATIVLEPIGITYM
QY         121         IINYLGHCISLVALLVAPVLFLRRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR         180           Db         81         IINYLGHCISLVALLVAFVLFLRL	358 325
QY 181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC 240	Oy 418 ARVAAMSITEYSENESTAN 444  DD 385 VPVARAMSIPTSPTRISFHGIKQTAAV 411
OY 241 YLHTAIVLTYSTDRLRKWMFICIGWGVPPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300	REGULT 6 149149 CRF receptor - mouse
Qy 301 YQGPMILVLLINFIFLENIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360 	Cippecies: wild musculus (nouse mouse) Cipate: Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004 CiAccession: Id-19149 RiPerrin, M.; Donaldson, C.; Chen, R.; Blount, A.; Berggren, T.; Bilezikjian, L.; Sawcher
Qy 361 VNPGEDEVSRVVFIYFNSFLESPQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420	Proc. Natl. Acad. Sci. U.S.A. 92, 2969-2973, 1995 A,Title: Identification of a second corticotropin-releasing factor receptor gene and chan A,Reference number: I49149; MUID:95224061; PMID:7708757 A,Accession: I49149
Oy 421 ARAMSIPTSPTRVSFHSIKQSTAV 444 	A;Status: preliminary; translated from GB/EMBL/DDBU A;Molecule type: mRNA A;Molecule type: mRNA A;Mesidues: 1-431 <res> A;Residues: 1-431 <res> A;Cross-references: UNIPROT:Q60748; UNIPARC:UPI0000028473; EMBL:U17858; NID:g727254; PIDN C;Superfamily: glucagon receptor</res></res>
RESULT 5 A55610 corticotropin-releasing factor receptor subtype 2 - rat	Query Match Best Local Similarity 62.4%; Score 1543; DB 2; Length 431; Best Local Similarity 62.4%; Pred. No. 3e-126; Matches 287; Conservative 59; Mismatches 64; Indels 50; Gaps 7;
	2 GGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCN
R;Lovenberg, T.W.; Liaw, C.W.; Grigoriadis, D.B.; Clevenger, W.; Chalmers, D.T.; De Souz Proc. Natl. Acad. Sci. U.S.A. 92, 836-840, 1995	5 GSLPSAQLLLCLFSLLPVLQVAQPGQAPQDQPLWTLLEQYCHRTTI-GNFSGPYTYCN
A.Title: Cloning and characterization of a functionally distinct corticotropin-releasing A; Reference number: A55610; MUID:95148632; PMID:7846062 A; Accession: A55610; MUID:95148632; PMID:7846062 A; Accession: A55610; A; Accession: A55610; A; A; Accession: A55610; A; A; Accession: A55610; A;	OY 46 ASVDLIGICMPRSPACQLVVRPCPAFFIGVRITINGIRECLANGSWAARVNISECQEL LUS
A;Setatus: preliminary; translated from GB/EMBL/DDBJ A;Setatus: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-411 <lov> A;Residues: 1-411 <lov> A;Cross-references: UNIPROT:P47866; UNIPARC:UPI000012842E; EMBL:U16253; NID:g644771; PIC</lov></lov>	Qy 106 LNB-EKKSKVHYHVAVIINYLGHCISLVALLVAFVLFIRLRPGCTHWGDQADGALEVGAP 164  :::  :  :  :  :                       Db 122 LDDKQRKYDLHYRIALIVNYLGHCVSVVALVAAFLLFL
C;Genetios: A;Gene: CRF2R C;Superfamily: glucagon receptor	Qy 165 WSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAY 224
Query Match 65.1%; Score 1550.5; DB 2; Length 411; Best Local Similarity 64.9%; Pred. No. 6.3e-127; Matches 290; Conservative 52; Mismatches 52; Indels 53; Gaps 6;	225
Qy 12 ALLLLGINPVSASIQDQHCESLSLASNISGLQCNASVDLIGTCWPRS 58 ,	Qy 285 EKCWFGKRPGVYTDYIYQGPMILVILINFIPLFNIVRILMTKIRASTTSETIQYRKAVKA 344
QY 59 PAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNE-EKKSKVHYH 117 	345 TLVLLPLLGITYMLFFVNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIR  345 TLVLLPLLGITYMLFFVNPGEDDSQIVFIYFNSFLESFQGFFVSVFYCFFNSEVRSAIR  332 TLVLLPLLGITYMLFFVNPGEDDLSQIVFIYFNSFLQSFQGFFVSVFYCFFNGEVRAALR

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RiJueppner, H.; Abou-Samra, A.B.; Freeman, M.; Kong, X.P.; Schipani, E.; Richards, J.; Kc Science 254, 1024-1026, 1991
Science 254, 1024-1026, 1991
A;Title: A G protein-linked receptor for parathyroid hormone and parathyroid hormone-relicable A;Reference number: A39286; WUID:92054592; PMID:1658941
A;Accession: A39286
A;Molecule type: mRNA
A;Residues: 1-431 KKIS-
A;Cross-references: UNIPROT:060748; UNIPARC:UPI000016CB13; BMBL:U21729; NID:g717137; PID:
C;Superfamily: glucagon receptor
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                                                                                                                                                                                                                                                               47 SVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 -----VLRSIRCLRNVIHWNLITTFILRNIAWFLLQL-IDHEVHEGNEVWCRCITTFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      226 YFHVTNFFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNE
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A;Cross-references: UNIPROT:P25107; UNIPARC:UP10000149EC4; GB:M74445
C;Superfamily: glucagon receptor
C;Superfamily: grotein-coupled receptor; transmembrane protein
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                                                                                                                               Length
                                                                                                                            63.8%; Score 1518.5; DB 2; Length
62.1%; Pred. No. 4e-124;
ive 58; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             406 RWHRWQDKHSIRARVARAMSIPTSPTRVSFHSIKQSTAV 444
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                                                                                                                                                      Best Local Similarity 62.19
Matches 285; Conservative
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                                                                                                                                                                                                oorticoliberin receptor precursor, cardiac - mouse
Cispecies: Mus musculus (house mouse)
Cispecies: Mus musculus (house mouse)
Cidate: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
Cidate: 21-Jul-1995 #sequence_revision 28-Jul-1995 #text_change 09-Jul-2004
Cidatesion: A56726
Ristenzel, P.; Kesterson, R.; Yeung, W.; Cone, R.D.; Rittenberg, M.B.; Stenzel-Poore, M.A. Stenzel, P.; Kesterson, R.; Yeung, W.; Cone, R.D.; Rittenberg, M.B.; Stenzel-Poore, M.A. Reference number: A56726; MulD:96015396; PMID:7565810
A;Accession: A56726
A;Grus: preliminary
A;Residues: 1-430 <STE>
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C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 09-Jul-2004
C;Accession: 149279
R;Kishishocto, T: Pearses, R.V.
Proc. Natl. Acad. Sci. U.S.A. 92, 1108-1112, 1995
A;Title: A sauvagine/corticotropin-releasing factor receptor expressed in heart and & A;Reference number: 149279
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 TTLDQIGTCWPQSAPGALVERPCPEYFNGIKYNTTRNAYRECLENGTWASRVNYSHCEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               46 ASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64.7%; Score 1540.5; DB 2; Length 430; 62.1%; Pred. No. 4.9e-126; ive 59; Mismatches 66; Indels 49;
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                               KRWHRWQDKHSIRARVARAMSIPTSPTRVSFHSIKQSTAV
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Keywords: cardiac muscle; heart
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Best Local Similarity 62.1%
Matches 285; Conservative
                            405
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	Query Match  23.3%; Score 554.5; DB 2; Length 593;  Best Local Similarity 31.6%; Pred. No. 3.4e-40;  Matches 131; Conservative 58; Mismatches 147; Indels 79; Gaps 12;  Qy 37 SNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSW 93  101 SRYGRPCLPEWDHI-LCWPLGAPGEVVAVPCPDYIYD-PNHKGHAYRRCDRNGSWELV 157  Qy 94AARVNYSECVKELTNETREREVPDYINVIGHCISLVALLVAFVLFIRLRPGCT 149  Db 158 PGHNRTWANYSECVKELTNETREREVPDRLGMIYTYGYSVSLASLTVA-VLIL 209  Qy 150 HWGDQADGALEVGAPPGPRESRICLRNIHHMLISAFILRNATWFV 200  Qy 201
ptor rmann, M	Oy 302 QGPMILVLLINFIFLENIVRILMTKLRASTTSETIQYRKAVKATLVLLPLGITYML 358
ons in the coding exoning in the coding exoning the coding exoning the coding exoning the coding in the coding cod	RESULT 11 S44203 paratyoid hormone-related peptide receptor - mouse paratyoid hormone-related peptide receptor - mouse C;Species: Mus musculus (house mouse) C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 C;Accession: S44203 R;Karperien, M.; van Dijk, T.B.; Hoeijmakers, T.; Cremers, F.; Abou-Samra, A.B.; Boonstration bubmitted to the EMBL Data Library, April 1994 A;Reference number: S44203 A;Reference number: S44203 A;Accession: S44203
; PIDN:AAA36525.1; PID	A;Status: preliminary A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 1-591 <kar> A;Cross-references: UNIPROT:P41593; UNIPARC:UPI0000027984; EMBL:X78936; NID:g474828; PIDR C;Superfamily: glucagon receptor C;Superfamily: glucagon receptor Cery Match Dest Local Similarity 31.6%; Pred. No. 3e-39; Matches 129; Conservative 63; Mismatches 143; Indels 73; Gaps 13;</kar>
A.Title: Clothing and functional expression of a human parathyroid hormone receptor. A.Reference number: 138113; MUID:93387403; PMID:8397094 A.Recession: 138113 A.Status: preliminary; translated from GB/EMBL/DDBJ A.Klatus: preliminary; translated from GB/EMBL/DDBJ A.Molecule type: mRNA A.Molecule type: mRNA A.Residues: 1-593 ARBZ> A.Residues: 1-593 ARBZ> A.Residues: 1-593 ARBZ>	41 GLQCNASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSW 105 GRPCLPEWDNI-VCWPLGAPGBEVVAVPCPDYIYDFNHKGHAYRRCDRNGSWEVVPGHN 94 AARVNYSECQEILNBEKKSKVHYHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGD
404/2;	Db 162 RTWANYSECLKFWITNETREREVFDRLGMIYTVGYSMSLASLTVA-VLIL 209  OY 154 QADGALEVGAPWSGAPPQVRRSIRCLENIIHWNLISAPILRNATWFVVQLTM 205  Db 210AYFRRLHCTRNYIHWHMFLSFWLRAASIFVKDAVLYSGFTLDE 252  OY 206SPEVHOSNVGWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVL 248  Db 253 ARRLTEBELHIIAQVPPPPAAAAVGYGCRVAVTFLYFLATNYYMILVEGLYLHSLIFM 312  OY 249 TYSTDRLRKWMFICIGWGVPPIIVAMAIGKLYYDNEKXFGRGRGCYTDYIYQGPMILV 308  Db 313 AFFSEKKXLMGFTIFGWGLPAVFVAVWVGVRATLANTGCWDLSSGHKKWHIQVPILAS 370

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A, Cross-treferences: UNTPARC:UP100000053A, EMBL:U10635, NID:g505752, PIDN:AAB48185.1, PII C, Superfamily: glucagon receptor G, Superfamily: glucagon receptor G, Superfamily: glucagon receptor glycoprotein, intestine, transmembrane protein coupled cside cside cside G, Sp. 1-35) Domain: signal sequence #status predicted cside cside
                                                                                                                                                                                                                                                                                                        a novel receptor for vasoactive
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A; Residues: 1-459 < LISH)
A; Residues: 1-459 < LISH)
A; Cross-references: UNIPROT: P30083; UNIPARC: UPI0000055A96; GB: M86835; NID: g207640; PI
A; Experimental source: lung
B; Pei, L.; Melmed, S.
Biochem. J. 308, 719-723, 1995
A; Title: Characterization of the rat vasoactive intestinal polypeptide receptor gene
A; Reference number: S56014; MUID: 97104266; PMID: 8948424
A; Accession: S56014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            273 IWTVVRIYFEDFGCW------DIIINSSLWWIIKAPILLSILVNFVLFICIIRILVQ 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLRAST -- TSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFIYFNSFLESF 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100 SECQEILNEEKKSKVHYHVAVIINY-LGHCISLVALLVAFVLFLRRFGCTHWGDQADGA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- 164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 AWAIGKLYYDNEKCWFGKRPGVYTD-----YIYQGPMILVLLINFIFLFNIVRILMT 325
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                                                                                     C;Species: Rattus norvegicus (Norway rat)
C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C;Accession: JH0594; S56014
R;Ishihara, T.; Shigemoto, R.; Mori, K.; Takahashi, K.; Nagata, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 MWDNLTCWPTTPRQQAVVLDCPLIFQLFAPIHGYNISRSCTBEGWSQ-LEPGPYHIACGL
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29.5%; Pred. No. 1.2e-38;
live 80; Mismatches 149; Indels
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A;Title: Functional expression and tissue distribution of
A;Reference number: JH0594; MUID:92232309; PMID:1314625
                                            vasoactive intestinal peptide receptor precursor - rat
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QGFVVAILYCFLNGEVQAELRRKWRRW 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      parathyroid hormone/parathyroid hormone related-peptide receptor - rat
C;Species: Rattus norregicus (Norway rat)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: 154195; A42698
R;Pausova, Z.; Bourdon, J.; Clayton, D.; Mattei, M.G.; Seldin, M.F.; Janicic, N.; Rivier
Genomics 20, 20-26, 1994
A;Title: Cloning of a parathyroid hormone/parathyroid hormone-related peptide receptor (and rat genomes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Cross-references: UNIPROT: P25961; UNIPARC: UP100001329C2; GB:L19475; NID: 9467316; PIDN: R;Abou-Samra, A.B.; Juppner, H.; Force, T.; Freeman, M.W.; Kong, X.F.; Schipani, E.; Ure Proc. Natl. Acad. Sci. U.S.A. 89, 2732-2736, 1992
A;Title: Expression cloning of a common receptor for parathyroid hormone and parathyroid nof both cAMP and inositol trisphosphates and increases intracellular free calcium.
A;Reference number: A42698; MUID:92212903; PMID:1313566
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                                                 371 VVLNFILFINIIRVLATKLRETNAGRCDTRQQYRKLLRSTLVLVPLFGVHYTVFWALP-Y 429
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 QADGALEVGAPWSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTM----- 205
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309 LLINFIFLFNIVRILMTKLR---ASTTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGE 365
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                                                                                                                                                                                                                                         430 TEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRW 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               366 DEVSRVVF---IYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRW 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 430 TEVSGTLWQIQMHYEMLFNSFQGFFVAIIYCFCNGEVQAEIRKSWSRW 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: A42698
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-565,'G','S87-591 <ABO>
A;Cross-references: UNIPARC:UPI00001789A7
A;Experimental source: ROS 17/2.8 osteosarcoma cells
A;Note: sequence extracted from NCBI backbone (NCBIE:92187)
C;Superfamily: glucagon receptor
                                                                                                                                                                      366 DEVSRVVF---IYPNSFLESPQGFFVSVPYCFLNSEVRSAIRKRWHRW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Mismatches 143;
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A;Residues: 1-591 <RES>
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22.8%; Score 543.5; DB
Best Local Similarity 31.6%; Pred. No. 3e-39;
Matches 129; Conservative 63; Mismatches 1.
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74

Gaps

Indels 109;

Mismatches 154;

64;

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212 KVG-CKLVMIFFQYCIMANYAWILVEGLYLHTILAISFFSERKYLQAFVLLGWGSPAIFV 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               329 TRGSETNHYKRLAKSTLLLIPLRGIHYIVFAPSP-EDAME--VQLFFELALGSFQGLVVA 385
                                                                                                                                                                                75 ----CWPSSAPARTVEVQCPKFLLMLSNKNGSLFRNCTQDGWSETFPRPDLACGVNINNS 130
                                                                                                                                                                                                                                                                                                                                                          213 NVGWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGVPFPII 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 VAWAIGKLYYDNEKCW-FGKRPGVYTDYIYQGPMILVLLINPIFLFNIVRILMTKLRAST 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T--SETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFIYFNSFLESFQGFFVS 389
                                                                                                                                                                                                                            103 QBILINEEK----KSKVHYHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       386 VLYCPINGEVQLEVQKKWRQWHLQEPPLRPVAFNNSFSNATNGPTHSTKASTEQSRSIP 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            390 VPYCFLNSEVRSAIRKRWHRWQ-------DKHSIRARVARAMSIP 427
                                                                       7 IRLVKALLLLGLNP----VSASLQDQ--HC-ESLS------LASNISGLQCNASVD
                                                                                                                                    50 LIGTCWPRSPAGOLVVRPCPAFFY-----GVRYNTTNNGYRECLANGSWAARVNYSEC
                                                                                                                                                                                                                                                                           131 ---FNERRHAYLLKCKVMYTV-----GYSSSLAMLLVALSIL-----CSF-----
                                                                                                                                                                                                                                                                                                                          158 ALEVGAPWSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFV--VQLTMSPEV---HQS
Conservative
152;
Matches
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                                                                                 R;Zolnierowicz, S.; Cron, P.; Solinas-Toldo, S.; Fries, R.; Lin, H.Y.; Hemmings, B.A. J. Biol. Chem. 269, 19530-19538, 1994
A;Ttele: Isolation, characterization, and chromosomal localization of the porcine calcid A;Reference number: A53972; MUID:94308241; PMID:8034723
A;Stcession: I47130
A;Status: preliminary.
                                                                                                                                                                                                                                                                                                                                                     PII
                                                                                                                                                                                                                                                                                                                            Residues: 1-498 <2OL>
;Cross-references: UNIPROT:P25117; UNIPARC:UP10000126878; EMBL:Z31356; NID:g531126;
                                                                                                                                                                                                                                                                                                                                                                                              A;Introns: 17/3; 70/1; 107/1; 144/3; 175/2; 233/3; 285/1; 305/2; 327/3; 400/3; 414/3
C;Superfamily: glucagon receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GLYCNRTWD--GWSCWDDTPAGVLAEQYCPDYFPDFDAABKVTKYCGEDGDWYRHPESNI 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 SWAARVNYSECQEILNEE-KKSKVHYHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTH 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 -----YFNLLAPFNALLYPT-RSISCQRVTLHKNMFLTYVL-NSIIIIVHLVVIVPNG 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   268 PPPIIVAWAIGKLYYDNEKCWFGKRPGVYTD--YIYQGPMILVLLINFIFLFNIVRILMT 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 PLIPTTAHAITRAVLFNDNCWL----SVDTNLLYIIHGPVMAALVVNFFFLLNILRVLVK 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   326 KLRASTTSETIQYRKAVKATLVLLPLLGITYMLFFVNPGEDEVSRVVFIYFNSFLESFQG 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 GLOCNASVDLIG-TCWPRSPAGQLVVRPCPAFF--YGVRYNTT-----NNGYRECLANG 91
                                                                  calcitonin receptor-1b - pig
C;Species: Sus acrofa domestica (domestic pig)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I47130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 EVHOSINGWCRLVTAAYNYFHVTNPFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22.4%; Score 533; DB 2; Length 498; 32.0%; Pred. No. 2e-38;
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Matches 129; Conservative 84; Mismatches 142; Indels
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                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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Search completed: March 16, 2006, 17:21:00 Job time : 43 secs

A;Molecule Type: mRNA A;Residues: 1-49 < -ISH3 A;Cross-references: UNIPROT:P23811; UNIPARC:UPI000013569A; EMBL:X59132; NID:G57228; PIDN C;Superfamily: glucagon receptor C;Keywords: G protein-coupled receptor; transmembrane protein

Status: preliminary

Score 531.5; DB 2; Length 449; Pred. No. 2.5e-38;

22.3%; 31.7%;

Query Match Best Local Similarity

C;Accession: S16319
R;Ishihara, T.; Nakamura, S.; Kaziro, Y.; Takahashi, T.; Takahashi, K.; Nagata, S.
EMBO 0. 10, 1635-1641, 1991
A;Title: Wolecular cloning and expression of a cDNA encoding the secretin receptor.
A;Reference number: S16319; WUID:91266890; PMID:1646711

Species: Rattus norvegicus (Norway rat) .Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 09-Jul-2004

secretin receptor - rat

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5.1.7
Biocceleration Ltd.
GenCore version
Copyright (c) 1993 - 2006
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OM protein - protein search, using sw model

Run on:

March 16, 2006, 17:13:03 ; Search time 231 Seconds (without alignments) 1356.080 Million cell updates/sec

US-10-649-193-15 2381

1 MCGHPQLRLVKALLLLGLNP......SIPTSPTRVSFHSIKQSTAV 444 Title: Perfect score: Seguence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

2166443 seqs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt\_05.80:\*
1: uniprot\_sprot:\*
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	рошо	рошо	homo	Q76118 macaca mula	Q8wmm0 tupaia glis	_	Q8k3r2 mesocricetu	P35353 rattus norv	Q9bgu4 bos taurus				Q8awa2 oncorhynchu	042602 xenopus lae		Q7t389 fugu rubrip		Q4jht0 cercopithec			gallus	Q8wml8 tupaia glis	oncorh		Q8wml9 tupaia glis		Q13324 homo sapien		_		Q5g124 mus musculu
ΩI	CRFR1 HUMAN	Q8NG71 HUMAN	Q4QRJ1_HUMAN	Q76LL8 MACMU	Q8WMMO_TUPGB	CRFR1 MOUSE	Q8K3R2 MESAU	CRFR1 RAT	Q9BGU4 BOVIN	CRFR1 SHEEP	CRFR1 CHICK	Q98UCZ 9TELE	Q8AWA2 ONCKE	CRFR1 XENLA	Q68Y61 RANCA	Q7T3S9_FUGRU	Q98UC0 9TELE	Q4JHT0_CERAE	Q5GH80_ONCMY	Q70JV6_CYPCA	Q7ZZZZ_CHICK	Q8WML8_TUPGB	Q8AWA1 ONCKE	Q98UC1_9TELE	OSWML9 TUPGB	CRFR2 RAT	CRFR2 HUMAN	Q4QRJ4 HUMAN	CRFR2 MOUSE	CRFR2_XENLA	Q5GL24 MOUSE
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% Query Match	100.0	97.6	91.8	91.2	90.2	89.8	89.4	89.3	89.3	87.6	81.7	76.3	75.8	75.5	75.1	74.1	73.1	70.4	68.5	67.9	67.3	66.4	66.2	65.6	65.5	65.1	65.1	65.1	64.8	64.7	64.3
Score	2381	2324	2186.5	2172.5	2146.5	2137.5	2128.5	2126.5	2126.5	2086.5	1945	1817.5	1804	1796.5	1789	1765	1741.5	1676.5	1631	1617.5	1603.5	1580	1576.5	1561	1559	1550.5	1549.5	1549.5	1543	1541.5	1530.5
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			Q4v3e9 drosophila Q7q773 anopheles g Q9v716 drosophila	Q9v6c7 drosophila Q65as2 nilaparvata Q65as3 nilaparvata
Q68Y60 RANCA Q4S8L0_TETNG	QSEIZI BEICO QBBJD9 MOUSE Q95L49 BOVIN	DIHR ACHDO Q5J877_ONCMY Q7TSA2_MESAU	Q4V3E9_DROME Q7Q773_ANOGA Q9V716_DROME	Q9V6C7_DROME Q65AS2_9HEMI Q65AS3_9HEMI
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411 501	277	441 150 154	475 454 504	388 641 631
			27.8 27.8 27.8	27.4 26.8 26.7
1515.5	743.5	703 686 663.5	663 662.5 662.5	651.5 638 635
33	9 9 9 4	33 39	4 4 4 4 1 2 2	4 4 4 5 4 3

## ALIGNMENTS

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CARTALINGAN

P349998; Q13008; Q9UK64;

01-FEB-1994 (Rel. 28, Created)

10-MAY-2005 (Rel. 28, Last sequence update)

10-MAY-2005 (Rel. 47, Last annotation update)

Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)

(Corticotropin-releasing hormone receptor 1) (CRH-R 1).

Name-CRHR; Synonyms-CRFR, CRFR1, CRHR;

Homo sapiens (Human)

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLBOTIDE SEQUENCE (ISOFORM CRF-R4).
MEDLINE=20065650; PubMed=10598591; DOI=10.1210/me.13.12.2189;
Grammatopoulos D.K., Dai Y., Randeva H.S., Levine M.A., Karteris E.,
Easton A.J., Hillhouse E.W.;
A novel spliced variant of the type 1 corticotropin-releasing hormone
receptor with a deletion in the seventh transmembrane domain present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE (ISOFORM CRF-R3).

TISSUE=Hippocampus;

MEDLINE=95110332; PubMed=7811272;

Ross P.C., Kostas C.M., Ramabhadran T.V.;

"A variant of the human corticorropin-releasing factor (CRF) receptor:
cloning, expression and pharmacology.";

Biochem. Biophys. Res. Commun. 205:1836-1842(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=98434465; PubMed=9757017; DOI=10.1016/S0378-1119(98)00322-9;
Sakai K., Yamada M., Horiba N., Wakui M., Demura H., Suda T.;
"The genomic organization of the human corticotropin-releasing factor type-1 receptor.";
Gene 219:125-130(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V; Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M., le Fur G., Caput D., Ferrara P.; "Primary structure and functional expression of mouse pituitary and human brain corticotrophin releasing factor receptors."; FEBS Lett. 335:1-5(1993).
                                                                                                                                                                                                                                                                                                                MUCLEOTIDE SEQUENCE [MRNA] (ISOFORMS CRF-R1 AND CRF-R2).
TISSUBE_Pituitary;
MEDLINE=94,022296; PubMed=7692441;
MEDLINE=94,022296; PubMed=7692441;
TEMPLE R., Lewis K.A., Perrin M.H., Vale W.W.;
"Expression cloning of a human corticotropin-releasing-factor
                                                                                                                                                                                                                                                                                                                                                                                                                     receptor.";
Proc. Natl. Acad. Sci. U.S.A. 90:8967-8971(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE [MRNA] (ISOFORM CRF-R2).
                                     444 AA.
                                     PRT;
                                     STANDARD;
                                                                                                                                                                                                                                                         Homo.
NCBI_TaxID=9606;
                                       HUMAN
RESULT 1
CRFR1 HUMAN
ID CRFR1 1
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GO; GO:0005886; C:plasma membrane; TAS.

GO; GO:0015056; F:corticotrophin-releasing factor receptor ac. .; TAS.

GO; GO:001190; P:ademylate cyclase activation; TAS.

GO; GO:0007189; P:G-protein coupled receptor protein signalin. .; TAS.

RO; GO:0007188; P:G-protein signaling, coupled to cAMP nucleo. .; TAS.

GO; GO:0007565; P:parturition; TAS.

GO; GO:0007565; P:parturition; TAS.

GO; GO:0007565; P:parturition; TAS.

GO; GO:0007565; P:parturition; TAS.

RO; GO:0007565; P:parturition; TAS.

GO; GO:0007567; P:parturition; TAS.

RO; GO:0007667; P:parturition; P:parturition; Receptor;

ROSITE; PSSO0659; G-PROTEIN RECEP F2. 1; 1.

ROSITE; PSSO0659; G-PROTEIN RECEP F2. 4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GQLVVRPCFARFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLQCNASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTN
-> D (in isoform CRP-R3).
FYIId-VSP 001996.
Missing (in isoform CRP-R2, isoform CRP-R3 and isoform CRP-R4).
FYIId-WSP 001997.
Missing (in isoform CRP-R4).
FYIId-VSP_001998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Corticotropin releasing factor receptor
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Cytoplasmic (Potential).
N-linked (GlcNAc. .) (Potential).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (Potential).
Cytoplasmic (Potential).
Extracellular (Potential).
5 (Potential).
Cytoplasmic (Potential).
6 (Potential).
Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
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SIGNAL 1 23
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                                                                                                                                                                                                                                         YEAUTH SEQUENCE OF 24-31, AND DISULFIDE BONDS.

X PubMed=1142585; DOI=10.1074/jbc.M101838200;

A Perrin M.H., Fischer W.H., Kunitake K.S., Craig A.G., Koerber S.C.,

Cervini L.A., Rivier J.B., Groppe J.C., Greenwald J.,

Moller Nielsen S., Vale W.W.;

Moller Nielsen S., Vale W.W.;

The first extracellular domain of the human type 1 corticotropin

T releasing factor receptor.";

L J. Biol. Chem. 276:31528-31534 (2001).

J. Biol. Chem. 276:31528-31534 (2001).

G. Howe high-affinity CRF binding. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.

C -1- SUBCELLULAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isold=P34998-3; Sequence=VSP 001996, VSP 001997;
Note=Does not bind to CRF with high affinity;
Name=CRF-R4; Synonyms=1D;
Isold=P34998-4; Sequence=VSP 001997, VSP 001998;
-1. TISSUB SPROTPICITY: Predominantly expressed in the cerebellum, pituitary, cerebral cortex and olfactory lobe.
-1. PTM: May be phosphorylated on Ser or Thr residues present in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C-terminal part.
-i- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                         King M.M., Aronstam R.S., Sharma S.V.; acDNs clones of human proteins involved in signal transduction sequenced by the Guthric cDNA resource center (www.cdna.org)."; Submitted (NOV-2003) to the EMBL/GenBank/DDBJ databases.
       in the human pregnant term myometrium and fetal membranes."; Mol. Endocrinol. 13:2189-2202(1999).
                                                                               NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA] (ISOFORM CRF-R2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L23333; AAA35719.1; -; mRNA.
EMBL; L23332; AAA35718.1; -; mRNA.
EMBL; K72304; CAA51052.1; -; mRNA.
EMBL; K703951; AAC6993.1; -; Genomic DNA.
EMBL; AF039510; AAC6993.1; -; Genomic DNA.
EMBL; AF039511; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039513; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039513; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039514; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039515; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039516; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039519; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039519; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039519; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039521; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039511; AAC6993.1; JOINED; Genomic DNA.
EMBL; AF039511; AAC6993.1; JOINED; GENOMIC DNA.
EMBL; AF180301; AAC6993.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Event=Alternative splicing; Named isoforms=4; Name=CRF-R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isold=P34998-2; Sequence=VSP_001997;
Note=Major isoform;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P34998-1; Sequence=Displayed;
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PIR, 160975; A48260
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(Potential).
(Potential).
(Potential).

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NCBI_TaxID=9606;
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A Subtract of the EMBL/GenBank/DDBJ databases.

B Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AB065867; BAC06179.1: -; Genomic DNA.

GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:000430; F:G-protein coupled receptor activity; IEA.

GO; GO:000430; F:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR003052; CRFI_receptor.

InterPro; IPR003051; CRF_receptor.

InterPro; IPR003051; CRF_receptor.

InterPro; IPR001879; horm_receptor.

R InterPro; IPR001879; horm_receptor.

R Pfam; PF020193; HRM; 11.
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                                                        180
                                                                                                                                                                                                                          241 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini, Hominidae,
                                121 IINYLGHCISLVALLVAFVLFIRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
                                                                                                                                                                                                                                                             241 YLHTAIVLTYSTDRLRKAMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRFGVTDYI
  IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
                                                                                                                NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                181 NIHWNLISAFILRNATWEVVQLTMSPEVHQSNVGWCRLVTAAXNYFHVTNPFWMFGEGC
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Last annotation update)
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PRINTS; PR01279; CRFRECEPTOR.
PRINTS; PR00249; GPCRECEPTOR1.
PRINTS; PR00249; GPCRECERTIN.
SMART; SM00008; HORMR; 1.
PROSITE; PS00649; G_PROTEIN RECEP F2_1; 1.
PROSITE; PS50027; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
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01-OCT-2002 (TrEMBLrel. 22, Last seq
01-UN-2003 (TrEMBLrel. 24, Last ann
Seven transmembrane helix receptor.
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Q8NG71;
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Matches 433; Conservative
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SEQUENCE 447 AA; 510
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TISSUB-G-protein coupled receptors;

WEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RATABLE R.L., Feligold B.A., Grouse L.H., Derge J.G.,

RIAUSDER R.L., Zeeberg B., Wagner L., Shemmen C.M., Schuler G.D.,

Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

Datchenko, L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton B., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;

""" "Generation and initial analysks of more than 15,000 full-length human
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                                                                                  FFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNBEKKSKVHYHVAVIINYLGHCIS 130
                                                                                                                                  LVALLVAFVLFLRERPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLRNIIHWNLISA 190
                                                                                                                                                                                                                                                                                                194 FILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTY 253
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RALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQLVVRPCPA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                          PILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31, Created)31, Last sequence update)31, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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NIH MGC Project;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q4QRJ1;
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
13-SEP-2005 (TrEMBLrel. 31,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRVSFHSIKQSTAV 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRVSFHSIKQSTAV 444
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KALLLIGLNPVSASLQDQHCESLSLASNI SGLQCNASVDLIGTCWPRSPAGQLVVRPCPA

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PRINTS; PR01280; CRFRECEPTOR1
                                                                                                                                                                                                                                                                           Similarity
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Best Local (
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TUPGB
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

Is submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.

R MGJ (2016021) C:integral to membrane; IEA.

GO; GO:0016021; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.

R GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR003051; CRPI receptor.

InterPro; IPR003051; CRPI receptor.

InterPro; IPR003083; GPCR secretin.

InterPro; IPR003083; GPCR secretin.

InterPro; IPR003083; GPCR secretin.

InterPro; IPR003083; HRM; 1.

R Pfam; PF002793; HRM; 1.
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                                                                                                                                                                                                                                                                                                                            GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
                                                                                                                                                                                                                                                                                                                                                                        61 GQLVVRPCPAFFYGVRYNTINNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                          121 IINYLGHCISLVALLVAFVLFIRIRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      212 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 IINYLGHCISLVALLVAFVLFLRL---------RSIRCLR 151
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                                                                                                                                                                                                                         1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                                                                                                                                                                                                   1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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                                                                                                                                                                             Gabs
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05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Name=CRF1;
Macaca mulatta (Rhesus macaque).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Primates; Catarrhini;
Carcopithecidae; Carcopithecinae; Macaca.
                                                                                                                                                                           29;
                                                                                                                         2; Length 415;
                                                                                                                                                                        Indels
Submitted (JUN-2005) to the EMBL/GenBank/DDBJ databases
                                                                                                                    Query Match 91.8%; Score 2186.5; DB 2; Best Local Similarity 93.5%; Pred. No. 4.7e-173; Matches 415; Conservative 0; Mismatches 0;
                                                                      47671 MW; 81445283CCE34C6E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 392 ARAMSIPTSPTRVSFHSIKQSTAV 415
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                  EMBL; BC096836; AAH96836.1; -; mRNA.
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Q76LL8;
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                                                                        415 AA;
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                                                                        SEQUENCE
                                              Receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           332 VNPGEDEVSRVVFIYENSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MARHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 NIIHWNLISARILRNATWFVVQLTWSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 YOGPMILVLLINFIPLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                     1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     212 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI
                                                                                                                                                                                                                                                                                                                 Gaps
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Buarchontoglires, Scandentia, Tupaiidae, Tupaia.
                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                             2; Length 415;
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MEDLINE-99067019; PubMed-9851694;
Palchaudhuri M.R., Wille S., Mevenkamp G., Spiess J., Fuchs
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ422241; CAD19577.1; -; mRNA.
                                                                                                                                                                                                      415 AA; 47784 MW; 84C530DEC6DA97AD CRC64;
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Last annotation update)
                                                                                                                                                                                                                                      Score 2172.5; DB 2;
Pred. No. 6.9e-172;
2;
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PRINTS; PRO0249; GPCRSECRETIN.
SMART; SM00008; HOTMR; 1.
PROSITE; PS00649; G PROTEIN RECEP F2 1; 1.
PROSITE; PS00650; G PROTEIN RECEP F2 2; 1.
PROSITE; PS50227; G PROTEIN RECEP F2 3; 1.
PROSITE; PS50261; G PROTEIN RECEP F2 3; 1.
                                                                                                                                                                                                                                                                                                                 0; Mismatches
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01-MAR-2002 (TrEMBLrel. 20, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                          91.2%;
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Q8WMMO;
                                                                                                                                                                                                                                                                                                                 tches 413; Conservative
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NUCLEOTIDE SEQUENCE.
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Pfam; PF00002; 7tm 2; 1.
Pfam; PF02793; HRM; 1.
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SIGNAL 1
                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                      [2]
NUCLEOTIDE SEQUENCE
       NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211
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                                                                                                   .; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 YLHTAIVLTYSTDRLRKWMFVCIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI
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01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rouse)
10-MAY-2005 (Mouse)
10-MAY-2005 (Mouse)
11-MAY-2005 (Mouse)
12-MAY-2005 (Mouse)
13-MAY-2005 (Mouse)
14-MAY-2005 (Mouse)
15-MAY-2005 (Mouse)
16-MAY-2005 (Mouse)
17-MAY-2005 (Mouse)
18-MAY-2005 (Mouse)
1
R GO; GO:0016021; C:integral to membrane; IRA.

R GO; GO:0016020; C:membrane; IRA.

R GO; GO:0016020; C:membrane; IRA.

R GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; II

R InterPro; IPR003052; CRFI receptor.

InterPro; IPR003052; CRFI receptor.

InterPro; IPR003052; CRFI receptor.

InterPro; IPR003053; GRFI receptor.

INTERPRO; IPR003053; GRFI receptor.

INTERPRO; IPR003054; GRFI receptor.

R Pfam; PP002793; HRM; 1.

R PRINTS; PR00249; GPCRECEPTOR.

R PROSTITE; PR005649; GPRCRECEPTOR.

R PROSTITE; PS00649; GPRCRECEPTOR.

R PROSTITE; PS00650; GPROTEIN RECEP F2_2; 1.

R PROSTITE; PS00650; GPROTEIN RECEP F2_2; 1.

R PROSTITE; PS00650; GPROTEIN RECEP F2_2; 1.

R PROSTITE; PS00650; GPROTEIN RECEP F2_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 90.2%; Score 2146.5; DB 2; Best Local Similarity 91.7%; Pred. No. 1e-169; Matches 407; Conservative 3; Mismatches 5;
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P35347;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Ensembl; ENSKUGG0000018634; Mus musculus.

Ensembl; ENSKUGG0000018634; Mus musculus.

Ensembl; ENSKUGG00000018634; Mus musculus.

GO; GO:0005615; C:extracellular space; TAS.

GO; GO:0015056; F:corticotrophin-releasing factor receptor ac. . .; IMP.

GO; GO:0007610; P:cesponse to stress; IMP.

InterPro; IPR003052; CRPI receptor.

InterPro; IPR003051; CRPI receptor.

InterPro; IPR003051; CRPI receptor.

InterPro; IPR001879; horm_receptor.
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PRINTS; PRO1280; CRERECEPTORI.
PRINTS; PRO049; GPCRSECRETIN.
SMART; SM00008; Horme; 1.
PROSITE; PS00649; G_PROTEIN RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN RECEP_F2_3; 1.
PROSITE; PS5027; G_PROTEIN RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN RECEP_F2_3; 1.
G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
Corticotropin releasing factor receptor
TISSUE=Pituitary;
MEDLINE=94063063; PubMed=8243652; DOI=10.1016/0014-5793(93)80427-V;
Vita N., Laurent P., Lefort S., Chalon P., Lelias J.-M., Kaghad M.,
le Fur G., Caput D., Ferrara P.;
"Primary structure and functional expression of mouse pituitary and
human brain corticotrophin releasing factor receptors.";
FRBS Lett. 335:1-5(1993).
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Cytoplasmic (Potential).
2 (Potential).
Extracellular (Potential).
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Cytoplasmic (Potential).
4 (Potential).
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EMBL; AF483484; AAL90758.1; -; mRNA.
EMBL; AF483485; AAL90759.1; -; mRNA.
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61 GQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NI IHMNLISAFILKNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNPFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212 YLHTAIVPTYSTDRLKKRMFVCIGWGVPFPIIVAMAIGKLYYDNBKCWFGKRPGVTDYI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 VNPGEDEVSRVVFIYFNSFLESPQGFFVSVPYCFLNSEVRSAIRKRWHRWQDKHSIRARV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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R GO; GO:0016021; C:integral to membrane; IEA.

R GO; GO:0016020; C:membrane; IEA.

R GO; GO:004930; F:G-protein coupled receptor activity; IEA.

GO; GO:0004931; F:receptor activity; IEA.

GO; GO:0007186; F:G-protein coupled receptor protein signalin.

R GO; GO:0007186; F:G-protein coupled receptor protein signalin.

R InterPro; IPR003052; CRF1 receptor.

InterPro; IPR003052; CRF2 receptor.

InterPro; IPR003052; CRF7 receptor.

INTERPRO; IPR003052; CRF7 receptor.

INTERPRO; IPR003052; CRF7 receptor.

INTERPRO; IPR003052; CRF7 receptor.

INTERPRO; IPR003054; GRF secretin.

INTERPRO; IPR0049; GPCREEPTOR.

INTERPRO; IPR0049; GPCREEPTOR.

INTERPRO; IPR0049; GPCREEPTOR.

INTERPRO; IPR0049; GPCREEPTOR.

INTERPRO; IPR00649; GPCREEPTOR.

INTERPRO; IPR00649; GPCREERTER.

INTERPRO; IPR00649; GPCREERTER.

INTERPROSTIE; PS006649; GPCREERTER.

INTERPROSTIE; PS006649; GPCREERTER.

INTERPROSTIE; PS006649; GPCREERTER.

INTERPROSTIE; PS006659; GPCREERTER.

INTERPROSTIE; PS006659; GPCREERTER.

INTERPROSTIE; PS006659; GPCREERTER.

INTERPROSTIE; PS006659; GPCREERTER.

INTERPROSTIER; PS006659; GPCREERTER.

INTERPROSTIER.
                                                                                                                               protein signalin.
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01-JUN-1994 (Rel. 29, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Corticotropin releasing factor receptor 1 precursor (Corticotropin-releasing hormone receptor 1) (CRH-R.)
Name=Crhr1; Synonyms=Crhr;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89.4%; Score 2128.5; DB 2
90.8%; Pred. No. 3.1e-168;
iive 5; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Z
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CRFR1 RAT
1 D CRFR1 RAT
AC P35357,
DT 01-JUN-1994 (
DT 01-JUN-1994 (
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SEQUENCE
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammaila, Butheria, Buarchontoglires, Glires, Rodentia, Sciurognathi,
Muridas, Cricetinae, Mesocricetus.
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(Potential).
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(Potential).
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QBKSR27
QBC3R27
O1-OCT-2002 (TrEMBLrel. 22, Created)
O1-OCT-2002 (TrEMBLrel. 22, Last sequence update)
O1-UUN-2003 (TrEMBLrel. 24, Last annotation update)
Type-1 corticotropin-releasing hormone receptor alpha isoform.
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                                                                                           Extracellular (Potential).

(Potential).

(Tobential).

(Toplasmic (Potential).

N-linked (GlCNAC. .) (Pot
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Plearchik A.V., Slominski A.;
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AX034599; AAK59707.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                             ' similarity.
81423BDA6D1CA070 CRC64;
               Extracellular (Potential)
                                    S (Potential).

Cytoplasmic (Potential).

6 (Potential).

Cotential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 2137.5; DB 1
Pred. No. 5.6e-169;
                                                                                                                                                                                                                                                                                                                                                             By similarity.
By similarity.
By similarity.
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91.2%;
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Matches 405; Conservative
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Name=CRH-R1;
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MEDLINE=96278921; PubMed=8662941; DOI=10.1074/jbc.271.24.14519;
Taai-Morxis C.-H., Bucako E., Geng Y., Gamboa-Pinto A., Dufau M.L.;
"The genomic structure of the rat corticotropin releasing factor receptor. A member of the class II G protein-coupled receptors.";
J. Biol. Chem. 271:14519-14525(1996).
                                                                                                                                                                                                                                                          STRAIN-Sprague-Dawley;
MEDLINE=94099969; PubMed=8274282; DOI=10.1016/0896-6273(93)90230-0;
Chang C.P., Pearse R.V. II, O'Connell S., Rosenfeld M.G.;
"Identification of a seven transmembrane helix receptor for corticotropin-releasing factor and sauvagine in mammalian brain.";
Neuron 11:1187-1195(1993).
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MEDLINE=21451158; PubMed=11567096; DOI=10.1110/ps.12101;
Hofmann B.A., Sydow S., Jahn O., van Werven L., Liepold T., Eckart
                                                                STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=94062694; PubMed=8243338; DOI=10.1210/en.133.6.3058;
Perxin M.H., Donaldson C.J., Chen R., Lewis K.A., Vale W.W.;
"Cloning and functional expression of a rat brain corticotropin releasing factor (CRF) receptor.";
Endocrinology 133:3058-3061(1993).
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GO; GO: 0004930; F:G-protein coupled receptor activity; IDA.
GO; GO: 0007218; P:G-protein signaling, coupled to cAMP nucleo.
GO; GO: 0007218; P:G-protein signaling pathway; IDA.
InterPro; IPR003052; CRF1_receptor.
InterPro; IPR0003051; CRF_receptor.
InterPro; IPR000351; GPCR_secretin.
InterPro; IPR001879; hormn_receptor.
PANTHER; PTHR12011:SF16; CRF_receptor; 1.
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L. U53487; AAC55519.1; JOINED; Genomic DNA.
L. U53488; AAC55519.1; JOINED; Genomic DNA.
L. U53499; AAC55519.1; JOINED; Genomic DNA.
L. U53491; AAC5519.1; JOINED; Genomic DNA.
L. U53491; AAC5519.1; JOINED; Genomic DNA.
L. U53491; AAC5519.1; JOINED; Genomic DNA.
L. U53493; AAC5519.1; JOINED; Genomic DNA.
L. U53494; AAC5519.1; JOINED; Genomic DNA.
L. U53496; AAC5519.1; JOINED; Genomic DNA.
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EMBL; L25438; AAA16441.1; -; mRNA.
EMBL; U53498; AAC53519.1; -; Genomic_DNA.
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EMBL, US3492, AAC5351
EMBL, US3494, AAC5351
EMBL, US3494, AAC5351
EMBL, US3495, AAC5351
EMBL, US3495, AAC5351
EMBL, US3494, AAC5351
PIR, IS8144, IS8144
                                          NUCLEOTIDE SEQUENCE
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Pfam; PF00002; 7tm_2; 1.
Pfam; PF01279; TRRECEPTOR.
PRINTS; PR01279; CRFRECEPTOR.
PRINTS; PR01280; CRFRECEPTOR.
PRINTS; PR00249; GPCRSECRIN.
SMART; SMO0008; HormR; 1.
PROSITE; PS00680; GPROTEIN RECEP F2 1; 1.
PROSITE; PS5027; GPROTEIN RECEP F2 2; 1.
PROSITE; PS5027; GPROTEIN RECEP F2 3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2 3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2 3; 1.
SPACETIN COUPLED A RECEP F2 3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2 4; 1.
Signal; Transducer; Transmembrane.
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                                                                                                                                                                                                                                                    Corticotropin releasing factor receptor
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Cytoplasmic (Potential).

Extracellular (Potential).

7 (Potential).
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Extracellular (Potential).
3 (Potential).
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Cytoplasmic (Potential).
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Extracellular (Potential)
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5; Mismatches 7;
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N-linked
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415 AA;
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VNPGEDEVSRVVF1YFNSFLESFOGFFVSVFYCFLNSEVRSA1RKRWHRWODKHS1RARV
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Extracellular (Potential).
3 (Potential).
Cytoplasmic (Potential).
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InterPro; IPR003052; CRF1_receptor.
InterPro; IPR003051; CRF_receptor.
InterPro; IPR000832; GPCR_secretin.
InterPro; IPR001879; horm. receptor.
PANTHER; PTHR12011:8F16; CRF_receptor; 1.
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                                                                                                                                                      392 ARAMSIPTSPTRVSFHSIKQSTAV 415
                                                                                                                      421 ARAMSIPTSPTRVSFHSIKQSTAV 444
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Pfam; PF02793; HRM; 1.
                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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SIGNAL 1
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1122
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214
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062772;
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A Takata M., Sekikawa K.;

A Takata M., Sekikawa K.;

Takata M., Sekikawa K.;

Takata M., Sekikawa K.;

Bubmitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

BMBL; AB055434; BAB21864.1; -; mRNA.

GO; GO:0016022; C:integral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004930; F:integral to membrane; IEA.

InterPro; IPR003051; CRF Integral to membrane; IRA.

InterPro; IPR003051; CRF Integral to membrane; IPR000032; GRF InterPro; IPR003051; CRF Integral to membrane; IPR000032; GRF Integral to membrane; IPR000032; GRF Integral to membrane; IPR00003; Morman Integral to membrane; IP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 GQLVVRPCLVFFYGVRYNTTINNGYRECLANGTWAARVNYSECQEILSEEKKSKVHYHIAV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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                                                                                                                                                                                                                                                                                                                                                                        Bos taurus (Bovine).
Bukaryota, Metacoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Laurasiatheria, Cetartiodactyla, Ruminantia,
Pecora, Bovidae, Bovinee, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29;
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89.3%; Score 2126.5; DB 2; Length 415;
Best Local Similarity 90.5%; Pred. No. 4.6e-168;
Matches 402; Conservative 7; Mismatches 6; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         415 AA; 47754 MW; 4A54A3DCE6CF2319 CRC64;
                                                                                                                                                                                                                                01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
Corticotropin-raleasing hormone receptor.
                                                                                                                                                                              415 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS, PRO1279; CRFRECEPTOR.
PRINTS, PRO1279; CRFRECEPTORI.
PRINTS; PRO1249; GPCRSECRETIN.
SMART; SMO0008; HORMR; 1.
PROSITE; PSS00250; G PROTEIN RECEP F2 2; 1.
PROSITE; PSS0127; G PROTEIN RECEP F2 3; 1.
PROSITE; PSS0121; G PROTEIN RECEP F2 3; 1.
392 ARAMSIPTSPTRVSFHSIKQSTAV 415
                                                                                                                                                                           Q9BGU4_BOVIN PRELIMINARY;
Q9BGU4;
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                                                                                                                                                                                                                                                                                                                                                Name=CRFR;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
420
                                                 332 VNPGEDEVSRVVFIYENSFLESFOGFFVSVFYCFLNSEVRSAIRKRWHRWODKHSIRARV 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=99079328; PubMed=9863624; DOI=10.1016/S0303-7207(98)00157-9; MEDLINE=99079328; PubMed=9863624; DOI=10.1016/S0303-7207(98)00157-9; Meyers D.A., Trinh J.V., Myers T.R.; Structure and function of the ovine type 1 corticotropin releasing factor receptor (CRF1) and a carboxyl-terminal variant."; Mol. Cell. Endocrinol. 144:21-35(1998).

-1 FUNCTION: This is a receptor for corticotropin releasing factor. Shows high-affinity CRF binding. The activity of this receptor is mediated by G proteins which activate adenylyl cyclase.

-1 SUBCELLULAR LOCATION: Integral membrane protein.
-1 PTM: Carboxyl-terminal Ser or Thr residues may be phosphorylated.
-1 SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
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PRINTS; PRO1280; CRFRECEPTOR.

PRINTS; PRO1280; CRFRECEPTOR.

PRINTS; PRO1280; CRFRECEPTOR.

PROSITE; PS00649; G-PROTEIN RECEP_F2_1; FALSE_NEG.

PROSITE; PS5027; G-PROTEIN RECEP_F2_2; 1.

PROSITE; PS50261; G-PROTEIN RECEP_F2_3; 1.

PROSITE; PS50261; G-PROTEIN RECEP_F2_3; 1.

G-protein coupled receptor; Glycoprotein; Phosphorylation; Receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-DBC-1998 (Rel. 47, Last annotation update)
Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
(Corticotropin-releasing hormone receptor 1) (CRH-R 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ovis aries (Sheep).

Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Caprinae; Ovis.
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420 AA;
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                                                                                                                                                                                                                                                                                          121 IINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALBVGAPWSGAPFQVRRSIRCLR 180
                                                                                                                                                                                                                                                                                                                                                  211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      332 VNPGEDEVSRVVPIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 391
                                                                                                                                                                                                                  9
                                                                                                                                                                                                                            1 MGRRPQLRLYKALLLIGINSISASLQDQHCESLSLASNVSGLQCNASVDLNGTCWPQSPA 60
                                                                                                                                                                                                                 1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                                                                                                                                                                                                                                                                              181 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                         152 NIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
                                                                                                                                                                                                                                                                                                                                                                                                         YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF
                                                                                                                                                                                                                                                                                                                                                                             212 YLHTAVVLTYSTDRLRKWAFICIGWGVPFPIIVAWAIGKLYDNEKCWFGKRPGVYTDYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Corticocropin releasing factor receptor 1 precursor (CRF-R) (CRF1)
(Corticocropin-releasing hormone receptor 1) (CRH-R 1).
       Extracellular (Potential).

S (Potential).

Cytoplasmic (Potential).

Extracellular (Potential).

Cytoplasmic (Potential).

Cytoplasmic (Potential).

N-linked (GlorNac. .) (Potential).
                                                                                                                                                                                                29;
                                                                                                                                                                             87.6%; Score 2086.5; DB 1; Length 415;
                                                                                                                                                                                               10; Indels
                                                                                                                                                          FASF652D12B4CDC4 CRC64;
                                                                                                                                                                                      Pred. No. 9.6e-165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  420 AA
                                                                                                           N-linked (GlCN)
N-linked (GlCN)
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                      Best Local Similarity oc. 11, Mismatches Matches 194; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421 ARAMSIPTSPTRVSFHSIKOSTAV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           392 ARAMSIPTSPTRVSFHSIKOSTAV 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                           47559 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken)
415 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
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                                                                        CARBOHYD
                                                                                  CARBOHYD
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CRFR1 CHICK
ID CRFR1 CH
AC Q90812;
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the Buropean Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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MEDLINE=96107136; PubMed=8536612; DOI=10.1210/en.137.1.192;
Yu J., Xie L.Y., Abou-Samra A.-B.;
Wolecular clonding of a type A chicken corticotropin-releasing factor receptor with high affinity for urotensin I.";
Endocrinology 137.192-197(1996).
-!- FUNCTION: This is a receptor for corticotropin releasing factor. Shows high-affinity binding for urotensin I. The activity of this receptor is mediated by G proteins which activate adentyly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 GPRPALLLILPLLOAPLLWDSPVAASIOSOYCESLLPTTWHTGPQCNASVDLIGTCWPRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GGHPQLRLVKALL ---LLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRS
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Corticotropin releasing factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUMCELLUTAR LOCATION: Integral membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Potential).
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(Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00649; G_PROTEIN_RECEP_F2_1; 1.
PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; 1.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
G-protein coupled receptor; Glycoprotein; Receptor; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23; Indels
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Cytoplasmic (Potential).
Cytoplasmic (Potential).
Extracellular (Potential).
5 (Potential).
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Extracellular (Potential).
7 (Potential).
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8C5C992925F62316 CRC64;
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Extracellular (Potential)
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Cytoplasmic (Potential).
N-linked (GlCNAC. .) (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L41563; AAA96656.1; -; Genomic DNA.
Ensembl; ENSGALGO000000371; Gallus Gallus.
InterPro; IPR003052; CRF1 receptor.
InterPro; IPR001832; GPCR secretin.
InterPro; IPR01879; hormin receptor.
PANTHER; PTHR12011:SF16; CRF receptor; PANTHER; PTHR2011:SF16; CRF receptor; PFE THR TOTAL TOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    By similarity. By similarity.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PRO1279; CRFEGEPTOR.
PRINTS; PRO1280; CRFEGEPTOR1.
PRINTS; PRO0249; GPCRSECRETIN.
SMART; SMO0008; HOLTER; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48600 MW;
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Pobl S., Darlison M.G., Lederis K., Richter D.;
Rollsylle Brain;
Pobl S., Darlison M.G., Lederis K., Richter D.;
Rollsylle Brain;
Rollsylle G. (Mra.2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ277157; CAC81753.1; -; mRRA.

GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0016021; Cintegral to membrane; IEA.

GO; GO:0004930; F:G-protein coupled receptor activity; IEA.

GO; GO:0004930; F:G-protein coupled receptor protein signalin. .; IEA.

GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IRR003051; CRF receptor.

InterPro; IRR003051; GRF receptor.

InterPro; IRR008032; GRPL secretin.

InterPro; IRR008032; GRPL secretin.

Pram; PP00002; 7tm 2; 1.

Pram; PP00002; 7tm 2; 1.

PRINTS; PR01299; CRFRECEPTORI.

PRINTS; PR01299; CRFRECEPTORI.

PRINTS; PR00349; GPCRSECRFIN.

PRINTS; PR00349; GPCRSECRFIN.

PRINTS; PR00349; GPCRSECRFIN.
                                                                                                                                           66 SSNATGLFCNISIDGIGTCWPRSNAGEIVSRPCPETFLGVRYNTTNNVYRECLANGTWAK 125
                                                                                                                                                                                                               96 RVNYSECQEILNEEKKSKVHYHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQA 155
                                                                                                                                                                                                                                             156 DGALEVGAPWSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVG
                                                                                                                                                                                                                                                                                                                                                    216 WCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGVPFFIIVAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                         217 WCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTYSTDKLRKWLFICIGWCIPFPIIVAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276 AIGKLYYDNEKCWFGKRPGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRASTTSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AIGKLYYDNEKCWFGKRAGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRASTTSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           336 IQYRKAVKATLVLLPLLGITYMLPFVNPGEDBVSRVVPIYPNSFLESFQGFFVSVPYCFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 ASNISGLOCNASVDLIGICMPRSPAGOLVVRPCPAFFYGVRYNTINNGYRECLANGSWAA
                                                         29; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Actinopterygii, Neopterygii, Teleostei, Euteleostei,
Protacanthopterygii, Salmoniformes, Salmonidae, Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              397 NSEVRSAVRKRWHRRQDKHSIRARVARAMSIPTSPTRVSFHSIKQSSAV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSEVRSAIRKRWHRWODKHSIRARVARAMSIPTSPIRVSFHSIKOSTAV 444
          DB 2; Length 445;
                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBAMA2 ONCKE PRELIMINARY; PRT; 430 AA.
QBAMA2;
QBAMA2.
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Corticotropin-releasing factor receptor type 1.
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                                                            19;
  76.3%; Score 1817.5; DB 2
82.9%; Pred. No. 2.3e-142;
ive 22; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00649; G PROTEIN RECEP F2 1; UNK PROSITE; PS00650; G PROTEIN RECEP F2 2; 1. PROSITE; PS5027; G PROTEIN RECEP F2 3; 1. PROSITE; PS50261; G PROTEIN RECEP F2 4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oncorhynchus keta (Chum salmon)
Query Match 76.3%
Best Local Similarity 82.9%
Matches 339; Conservative
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                                      64 AVGQLVARPCPEYFYGVRYNTTNNGYRECLANGSWAARVNYSQCQEILSEEKRSKLHYHI 123
                                                                                                             119 AVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRC 178
                                                                                                                                  155 LRNIIHWNLITAPILRNATWFVVQLTMNPEVHESNVVWCRLVTAAYNYFHVTNFFWMFGE 214
                                                                                                                                                                                                                                                                                                                         GCYLHTAIVLTYSTDRLRKMMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTD 298
                                                                                                                                                                                                                                                                                                                                                    215 GCYLHTAIVLTYSTDKLRKWMPICIGWCIPPPIIVAWAIGKLYYDNEKCWPGKRAGVYTD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                 YIYQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYML 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        359 FFVNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 PAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQBILNEBKKSKVHYHV 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . ., IEA.
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MEDININE-21066341; PubMed=11145609; DOI=10.1210/en.142.1.446;
Arai M., Assil I.Q., Abou-Samra A.B.;
"Characterization of three corticotropin-releasing factor receptors in catfish: a novel third receptor is predominantly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                            275 YIYQGPMILVILINPIFIFNIVRILMTKLRASTTSETIQYRKAVKATLVILSLIGITYML
                                                                                                                                                                                                                  179 LRNIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    098UC27

01-UUN-2001 (TEMBLEE]. 17, Created)

01-UUN-2001 (TEMBLEE]. 17, Last sequence update)

01-UUN-2001 (TEMBLEE]. 17, Last sequence update)

01-MRA-2004 (TEMBLEE]. 26, Last annotation update)

Corticotropin releasing factor receptor 1.

Ameiurus nebulosus.

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

Ictaluridae, Ameiurus.

NGB_TAXID=27778;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pituitary and urophysis.";

Endocrinology 142:446-454 (2001).

Endocrinology 142:446-454 (2001).

Endocrinology 142:446-454 (2001).

Endo. GO:0016020; C:inegaral to membrane; IEA.

GO; GO:0016020; C:membrane; IEA.

GO; GO:0004930; F:G-protein coupled receptor activity; IEA.

GO; GO:0004872; F:receptor activity; IEA.

R GO; GO:0007186; P:receptor activity; IEA.

R GO; GO:0007186; P:receptor activity; IEA.

R InterPro; IPR000352; CRFI receptor.

InterPro; IPR000352; GRF receptor.

InterPro; IPR001051; CRF receptor.
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PRINTS, PRO1280, CRERECEPTOR.
SMANTS, PRO0249, GPCRSCERTIN.
BROSTIE, PRO0649, GPROTEIN RECEP F2_1; UNKNOWN_1.
PROSITE, PS00650, GPROTEIN RECEP F2_1; UNKNOWN_1.
PROSITE, PS00501, GPROTEIN RECEP F2_3; 1.
PROSITE; PS50261; GPROTEIN RECEP F2_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 445 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 RVARAMSIPTSPTRVSFHSIKQSTAV 444
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SEQUENCE
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65 VRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAVIINY 124
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use as long as its content is in no way modified and this statement is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 PCLLIVQ-VIAAGISFALTSLQDQ-CETLQHNSNFTGLACNASIDMIGTCWPSTAAGGWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  65 ARPCPEYFHGVQYNTTGNVYRECHLNGSWAGRGDYAQCQEILKQEKKTKVHYHIAIVINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125 LGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLRNIIH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         156 WNLITAFILRNVTWFVMQLTLSHEAHDSNVVWCRLVTIAHNYFYVTNFFWMFGEGCYLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 POLRLVKALLLLGINPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQLV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245 AIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYIYQGP
                                                                                                                                                                                                                                                                     Corticotropin releasing factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cytoplasmic (Potential).
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
N-linked (GlCNAc. .) (Potential)
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                              DB 1; Length 415;
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6 (Potential).
Extracellular (Potential).
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2 (Potential).
Extracellular (Potential).
3 (Potential).
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Extracellular (Potential).
5 (Potential).
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1 (Potential).
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                                                                                                                                                                                                                                                                                                                                                                     Cytoplasmic (Potential).
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By similarity.
By similarity.
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                                                                                                                                                                                                                                                          Potential
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                                                 4
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                                                                                                                       VDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILN 107
                                                                                                                                    63 IDPIGTCWPKSTAGEWVLRPCPEMFYGVKYNTTNNVYRECLSNGSWAVKGNYTQCQEILM 122
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                                                                                                                                                                                                                                                                                 213 HVTNFFWMFGEGCYLHTAIVLTYSTDKLRKWMFICIGWCIPLPIIIAWAIGKLYYDNEKC
                                                                       ---ISGLQCNAS
                                                                                      228 HVTNFFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKC
                                                                                                                                                                                                                                                                                                                     288 WFGKRPGVYTDYIYQGPMILVLLINPIFLFNIVRILMTKLRASTTSETIQYRKAVKATLV
                                                                                                                                                                                                                      168 APFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYF
                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUR=Brain;
MEDLINE=97465573; PubMed=9326293;
Dautzenberg F.M., Dietrich K., Palchaudhuri M.R., Spiess J.;
"Identification of two corticotropin-releasing factor receptors from Xenopus laevis with high ligand selectivity: unusual pharmacology of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: Belongs to the G-protein coupled receptor 2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Corticotropin releasing factor receptor 1 precursor (CRF-R) (CRFI)
(Corticotropin-releasing hormone receptor 1) (CRH-R 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
                                                20,
                      Query Match 75.8%; Score 1804; DB 2; Length 430; Best Local Similarity 74.2%; Pred. No. 2.9e-141; Matches 340; Conservative 36; Mismatches 32; Indels 5
49595 MW; BCD2CDF36B1281A2 CRC64;
                                                                       7 LRLVKALLLLGLNPVSASLQDQHCESLSLASN------
                                                                                                                                                                                                                                                                                                                                                                                                                                   393 WHRWQDKHSIRARVARAMSIPTSPTRVSFHSIKQSSAV 430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 AA
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430 AA;
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042602;
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Search completed: March 16, 2006, 17:20:15 Job time : 234 secs
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Submitted (Aug-2004) to the EMBL/GenBank/DDBJ databases.

EMBL, AB188110; BAD36783.1; -; mRNA.

GO; GO:0016021; C:integral to membrane; IRA.

GO; GO:0016020; C:membrane; IRA.

GO; GO:0004872; F:receptor activity; IRA.

GO; GO:0004872; F:receptor activity; IRA.

R GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; IEA.

InterPro; IPR0010352; CRFL-receptor.

R InterPro; IPR0010351; GRF receptor.

R InterPro; IPR001037; IRA receptor.

R InterPro; IPR001037; IRA receptor.

R InterPro; IPR001031; IRA receptor.

R InterPro; IPR001031; IRA receptor.

R InterPro; IPR001031; IRA receptor.

R Pfam; PF00002; Ytm 2; 1.
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                                                                                                                             62 QLVVR-PCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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                                                                                                 424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=CRFR-1;
Aman cateabelana (Bull frog).

Rukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Raniae; Rana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 416;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ito Y., Ogata D., Hasunuma I., Kikuyama S.;
molecular cloning of two corticotropin releasing factor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-OCT-2004 (TrEMBLrel. 28, Created)
25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Cortcotropin releasing factor receptor type 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                        416 AA
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PRINTS; PRO1280; CRFRECEPTORI.
PRINTS; PRO0249; GPCRSECRETIN.
SMART; SMO00009; HORMR; I.
PROSITE; PSO0650; G PROTEIN RECEP F2 2; I.
PROSITE; PS50227; G PROTEIN RECEP F2 3; I.
PROSITE; PS50221; G PROTEIN RECEP F2 4; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                     396 SIPTSPTRISPHSIKOSSAI 415
                                                                                                                                                                                                                     SIPTSPTRVSFHSIKQSTAV 444
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NCBI_TaxID=8400;
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300
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                            213 YLHTAIVLTYSTDKLKKMMFICIGWCIPPPIIVAWAIGKLYYDNGKCWFGKKAGVYTDFI
                                                                                                             YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF
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APPLICANT Chen, Ruoping
APPLICANT Chen, Ruoping
APPLICANT Chen, Ruoping
APPLICANT Lewis, Kathy A.

APPLICANT Lewis, Kathy A.

APPLICANT Lewis, Cathy A.

APPLICANT Sawchenko, Paul
TILE CP INVENTION: Cloning and Recombinant Production of
TILE REPRENCE: P41-90002

TILE REPRENCE: P41-90002

CURRENT APPLICATION CRF Receptor(8)

FILE REPRENCE: P41-90002

CURRENT FILING DATE: 1995-06-07

EARLIER PELIGATION NUMBER: US 08/374,009

EARLIER PELING DATE: 1995-01-17

EARLIER PILING DATE: 1995-01-17

EARLIER PILING DATE: 1994-12-09

EARLIER FILING DATE: 1994-05-25

EARLIER PILING DATE: 1993-06-23

EARLIER PILING DATE: 1993-06-23

EARLIER PILING DATE: 1993-06-23

EARLIER PILING DATE: 1993-06-28

EARLIER PILING DATE: 1993-06-18

SOFTWARE: FRANCE FREED for Windows Version 3.0

SEQ ID NO 15
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Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0;
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US-09-799-978-42

US-09-799-978-6

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US-08-981-401-2

US-08-981-401-2

US-08-981-401-4

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; Sequence 15, Application US/08482746B
; Patent No. 639915;
; GENERAL INFORMATION:
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                                           181 NIHHWNLISAFILRNATWFVVQLTMSPEVHQSNVGMCRLVTAAYNYFHVTNFFWMFGEGC
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| Sequence 15, Application US/08374009A
| Patent No. 6495343
| GENERAL INFORMATION:
| APPLICANT: Pertin, Marilyn H.
| APPLICANT: Chewis, Kathy A.
| APPLICANT: Vale Jr. Wylie W.
| APPLICANT: Vale Jr. Wylie W.
| APPLICANT: Vale Jr. Wylie W.
| APPLICANT: Sawchenko, Paul
| TITLE OF INVENTION: Cloning and Recombinant Production of TITLE OF INVENTION NUMBER: US 08/079,320
| EARLIER FILING DATE: 1993-06-18
| EARLIER FILING DATE: 1993-06-18
| EARLIER FILING DATE: 1993-06-23
| EARLIER FILING DATE: 1994-05-25
| NUMBER OF SEQ ID NOS: 15
| SOFTWARE: FESTSEQ for Windows Version 3.0
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100.0%; Pred. No. 1.2e-232;
ative 0; Mismatches 0;
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Best Local Similarity 100.
Matches 444; Conservative
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US-08-374-009-15
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181 NIIHWNLISAFILRNATWFVVQLTMSPBVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
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Patent No. 6482608

GRERRAL INFORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Vale Jr. Wylle W.
APPLICANT: Vale Jr. Wylle W.
APPLICANT: Sawchenko, Paul
ITILE OF INVENTION: Clouing and Recombinant Production of
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ITILE OF INVENTION: Clouing and Recombinant Production of
ITILE OF INVENTION: Clouing and Recombinant Production
FILE PROPERTY SPECIAL SAIRTY 8

CURRENT APPLICATION NUMBER: US/09/580,734

CURRENT APPLICATION NUMBER: US/09/191,724

PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-11-12
PRIOR PELING DATE: 1998-11-10
PRIOR PELING DATE: 1993-06-18

PRIOR FILING DATE: 1993-
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241 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
                                                                                                                                                                                                                                                                                                                                                                      Sequence 11, Application US/09631603

Sequence 11, Application US/09631603

Batent No. 6733990

GENERAL INFORMATION:
APPLICANT: Hodge, Martin R.
APPLICANT: Hodge, Martin R.
APPLICANT: Weich, Nadine
TITLE OF INVENTION: 15571, A NO. 6733990e1 GPCR-like Molecule of the
TITLE OF INVENTION: 5ecretin-Like Family and Uses Thereof
TITLE OP INVENTION Secretin-Like Family and Uses Thereof
FILE REPRENCE: 5800-484

CURRENT APPLICATION NUMBER: US/09/631,603

PRIOR APPLICATION NUMBER: 09/515,781

PRIOR APPLICATION NUMBER: 60/146,916

PRIOR FILING DATE: 2000-02-29

PRIOR FILING DATE: 2000-08-03

NUMBER OF SEQ ID NOS: 24

NUMBER OF SEQ ID NOS: 24

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                       301 YQGPMILVYLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLFLLGITYMLFF
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100.0%; Score 2381; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-232;
Matches 444; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                          ARAMSIPTSPTRVSFHSIKQSTAV 444
                                                                                                                                                                                                                                                 421 ARAMSIPTSPTRVSFHSIKQSTAV 444
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US-09-631-603-11
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                                                                                                                     301 YQCPMILVLLINFIPLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
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                             241 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
                                                                                                                                                                            361 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
                                                                                                                                                                                                            361 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
                                                                                           YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
    YLHTAIVLTYSTDRLRKWMPICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 300
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APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Vale Jr., Wylie W.
APPLICANT: Sawchenko, Paul
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: CRP Receptor(8)
FILE REFERENCE: Salk1748
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100.0%; Pred. No. 1.2e-232;
iive 0; Mismatches 0;
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CURRENT PILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER PILING DATE: 1998-10-17
EARLIER PILING DATE: 1995-01-17
EARLIER PILING DATE: 1994-12-09
EARLIER PEDILICATION NUMBER: US 08/35,537
EARLIER PEDILICATION NUMBER: PCT/US94/05908
EARLIER PILING DATE: 1993-06-25
EARLIER PILING DATE: 1993-06-23
EARLIER PILING DATE: 1993-06-18
EARLIER PILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASSEQ for Windows Version 3.0
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Patent No. 6638905
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Best Local Similarity 100.
Matches 444; Conservative
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ORGANISM: Homo sapiens
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361 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVPYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
                                                     301 YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 360
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  212 YLHTAIVLTYSTDRLRKWMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 271
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                                                                                  272 YQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLDFLGITYMLFF
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Pred. No. 5.7e-213;
0; Mismatches 0; Indels 29;
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APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Vale Jr.
APPLICANT: Vale Jr.
APPLICANT: Vale Jr.
APPLICANT: Vale Jr.
APPLICANT: Sawchenko, Paul
ITLE OF INVENTION: Cloning and Recombinant Production of
ITLE OF INVENTION: Cloning and Recombinant Production of
ITLE OF INVENTION: Cloning and Recombinant Production of
ITLE OF INVENTION: CRF Receptor(8)
FILE REFERENCE: P41-90002
CURRENT APPLICATION NUMBER: US 08/374,009
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-01-17
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1994-05-25
EARLIER APPLICATION NUMBER: US 08/110,286
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-06-18
EARLIER PILING DATE: 1993-06-18
EARLIER PILING DATE: 1993-06-18
EARLIER PILING DATE: 1993-06-18
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6399315
GENERAL INFORMATION:
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Best Local Similarity 93.5<sup>3</sup>
Matches 415; Conservative
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                                                                                                                                             Bequence 2, Application US/08110286A
Patent No. 5728545
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Use is, Walte W.
APPLICANT: Chen, Ruoping
ITILE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
ITILE OF INVENTION: CR RECEPTOR(S)
NUMBER OF SEQUENCES:
CORRESPONDENCES:
CORRESPONDENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 91.8%; Score 2186.5; DB 1; Length 415; Best Local Similarity 93.5%; Pred. No. 5.7e-213; Matches 415; Conservative 0; Mismatches 0; Indels 29;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
STRET: 444 South Flower Street, Suite 2000
CITY: Los Angeles
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/110,286A
421 ARAMSIPTSPTRVSFHSIKQSTAV 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,192
REPERENCE/DOCKET NUMBER: P41 9439
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEPHONE: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/079,320
FILING DATE: 18-UDM-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 415 amino acids
amino acid
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                                                                                                                                UNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV
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Sequence 2, Application US/08374009A

Patent No. 6495343

GENERAL INPORMATION:
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia W.
APPLICANT: Sawchenko, Paul
ITILE OF INVENTION: Cloning and Recombinant Production of
ITILE OF INVENTION: Cloning and Receptor(8)
FILE REFERENCE: P41 9886
CURRENT PILING DATE: 1995-01-17
EARLIER APPLICATION NUMBER: US 08/374,009A
CURRENT FILING DATE: 1995-01-17
EARLIER FILING DATE: 1994-01-09
EARLIER FILING DATE: 1993-06-18
EARLIER FILING DATE: 1993-06-18
EARLIER FILING DATE: 1993-06-18
EARLIER FILING DATE: 1993-06-18
EARLIER FILING DATE: 1993-06-25
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENDING: DATE: 1994-05-25
LENDING: DATE: 1994-05-25
LENDING: DATE: 1994-05-25
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US-08-374-009-2
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                                         272 YQGPMILVLIINPIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLFLLGITYMLFF
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                                                                                                                                   361 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV
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91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USCUSSION 1942

SEQUENCE 2, Application US/09580734
Fatent No. 6482608
GENERAL INFORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: CRF Receptor(8)
FILE REPERENCE: SAIK1748
CURRENT APPLICATION NUMBER: US/09/580,734
CURRENT FILING DATE: 1998-11-124
PRIOR PRILING DATE: 1998-11-1209
FRIOR APPLICATION NUMBER: US 08/374,009
FRIOR APPLICATION NUMBER: US 08/353,537
FRIOR APPLICATION NUMBER: US 08/353,537
FRIOR APPLICATION NUMBER: US 08/310,286
FRIOR APPLICATION NUMBER: US 08/110,286
FRIOR APPLICATION NUMBER: US 08/079,320
FRIOR APPLICATION NUMBER: US 08/079,320
FRIOR APPLICATION NUMBER: US 08/079,320
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FRIOR APPLICATION NUMBER: US 08/079,320
FRIOR APPLICATION NUMBER: US 08/110,286
FRIOR APPLICATION NUMBER: US 08/079,320
FRIOR FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
FRIOR FILING DATE: 1993-06-18
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ORGANISM: Homo sapiens
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US-09-580-734-2
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; ORGANISM: homo sapiens
US-09-799-978-2
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TYPE: PRT
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US-09-799-978-2
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US-09-799-978-4
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361 UNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWQDKHSIRARV 420
                        332 VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHRWODKHSIRARV 391
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Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29;
                                                                                                                                                                                                                                              APPLICANT: Chen, Ruching H.
APPLICANT: Chen, Ruching H.
APPLICANT: Chen, Ruching A.
APPLICANT: Chen, Ruching A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: CDIONING and Recombinant Production of
TITLE OF INVENTION: CDIONING and Receptor(8)
FILE REFERENCE: Salk148
CURRENT APPLICATION NUMBER: US/09/191,724
CURRENT FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-01-17
EARLIER FILING DATE: 1991-05-25
EARLIER FILING DATE: 1993-06-23
EARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FREESEQ for Windows Version 3.0
                                                                                            392 ARAMSIPTSPTRVSFHSIKQSTAV 415
                                                                       421 ARAMSIPTSPTRVSPHSIKQSTAV 444
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US-09-191-724-2
US-09-191-724-2
Pactent No. 6638905
GENERAL INFORMATION
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ORGANISM: Homo sapiens
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Sequence 2, Application US/0979978

Patent No. 6670140

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Sheldon, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass (TITLE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors
FILE REFERENCE: 8448
CURRENT APPLICATION NUMBER: US/09/799,978
CURRENT PILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
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91.8%; Score 2186.5; DB 2; Length 415;
Best Local Similarity 93.5%; Pred. No. 5.7e-213;
Matches 415; Conservative 0; Mismatches 0; Indels 29;
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Patent No. 6670140
GENERAL INPORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert
APPLICANT: Sheldon, Russell
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61 GQLVVRPCPAFFYGVRYNTTINNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAV 120
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                                                                                                  Gaps
                                                                                                  29;
                                                 DB 2; Length 415;
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patent No. 639315
GENERAL INPORMATION:
APPLICANT: Perrin, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Lewis, Kathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Sawchenko, Paul
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Receptor(s)
FILE REFERENCE: P41-90002
CURRENT APPLICATION WUMBER: US/08/482,746B
CURRENT APPLICATION NUMBER: US 08/374,009
EARLIER FILING DATE: 1995-06-07
EARLIER FILING DATE: 1994-06-07
EARLIER FILING DATE: 1994-12-09
EARLIER FILING DATE: 1994-06-25
EARLIER FILING DATE: 1994-05-25
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-08-23
EARLIER FILING DATE: 1993-08-18
EARLIER FILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASTSEQ FOR WINDOWS Version 3.0
                                                                                                  1; Indels
                                                 91.6%; Score 2180.5; DB 2
93.2%; Pred. No. 2.3e-212;
tive 0; Mismatches 1;
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                                              Query Match
Best Local Similarity 93.2°
Matches 414; Conservative
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US-08-482-746-13
  US-09-826-509-483
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US-08-482-746-13
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TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass
TITLE OF INVENTION: Punction Using Corticotropin Releasing Factor Receptors
FILE REFERENCE: 8448
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| Sequence 481, Application US/09826509
| Patent No. 6806054
| GENERAL INFORMATION:
| APPLICANT: Lehannan-Bruinsma, Karin
| APPLICANT: Liaw, Chen W.
| APPLICANT: Lin, I-Lin
| APPLICANT: Lin, I-Lin
| TITLE OF INVENTION: No. 6806054-Endogenous, Constitutively Activated Known G
| TITLE OF INVENTION: Protein-Coupled Receptors
| TITLE OF INVENTION NUMBER: 2001-04-05
| CURRENT PELING DATE: 2001-04-05
| PRIOR PILING DATE: 2000-04-07
| PRIOR PILING DATE: 2000-04-07
| PRIOR PILING DATE: 1998-10-13
| NUMBER OF SEQ ID NOS: 589
| SEQ ID NO 483
| MUMBER OF SEQ ID NOS: 589
| SEQ ID NO 483
| MUMBER OF SEQ ID NOS: 589
| SEQ ID NO 483
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                                                                                                                                                                                                                                                                                                                         Query Match 91.8%; Score 2186.5; DB 2; Length 415; Best Local Similarity 93.5%; Pred. No. 5.7e-213; Matches 415; Conservative 0; Mismatches 0; Indels 29;
                                                      CURRENT APPLICATION NUMBER: US/09/799,978
CURRENT FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
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US-09-799-978-4
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ORGANISM: Homo sapiens
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US-09-826-509-483
                                                                                                                                                                                               LENGTH: 415
TYPE: PRT
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Search completed: March 16, 2006, 17:21:53 Job time : 49 Becs
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                                                                                                                  1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                                Gaps
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        DB 2; Length 415;
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APPLICANT: Chen, Marilyn H.
APPLICANT: Chen, Ruoping
APPLICANT: Chen, Ruoping
APPLICANT: Lewis, Rathy A.
APPLICANT: Lewis, Rathy A.
APPLICANT: Donaldson, Cynthia J.
APPLICANT: Bawchenko, Paul
TILLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Cloning and Recombinant Production of
FILE OF INVENTION NUMBER: US 09/191,724
PRIOR APPLICATION NUMBER: US 08/334,009
PRIOR PILLING DATE: 1994-12-09
PRIOR APPLICATION NUMBER: US 08/110,286
PRIOR APPLICATION NUMBER: US 08/110,286
PRIOR PILLING DATE: 1993-06-18
PRIOR PILLING DATE: 1993-06-18
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Score 2137.5; DB 2
Pred. No. 5.3e-208;
4; Mismatches 6;
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     Query Match
Best Local Similarity 91.2%;
Matches 405; Conservative
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US-09-580-734-13
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                                                                                    1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                              Gaps
                                            29;
89.8%; Score 2137.5; DB 2; Length 415;
91.2%; Pred. No. 5.3e-208;
ive 4; Mismatches 6; Indels 29;
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    Query Match
Best Local Similarity 91.21
Matches 405; Conservative
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181 NIIHWNLISAFILRNATWFVVQLTWSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
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483, App
131, App
137, App
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22, Appl
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Sequence 15, Appl
Sequence 708, App
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Sequence 15, Appl
                                                                                                                March 16, 2006, 17:21:14 ; Search time 168 Seconds
   (without alignments)
   1104.263 Million cell updates/sec
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(cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

(cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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US-10-242-8228-2
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US-10-649-852-4
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Sequence 132, Application US/09853386

j Sequence 132, Application US/09853386

j Sequence 132, Application US/09853386

j Eatent No. US20020049151A1

j GENERAL INFORMATION:

j APPLICANT: Murphy, Evelyn

j APPLICANT: Conneely, Orla

j APPLICANT: Fitzgeraid, Oliver

j TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR

j TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

j TITLE OF INVENTION: US (199/853, 386

j CURRENT FILING DATE: 2001-05-11

p PRIOR APPLICATION NUMBER: US 60/203645

j PRIOR APPLICATION NUMBER: US 60/203645

j PRIOR PELING DATE: 2000-05-12

j NUMBER OF SEQ ID NOS: 153

j SOFTWARE: PatentIn version 3.1

j SED ID NOS: 153

j SOFTWARE: PatentIn version 3.1
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                              Sequence 16, Appl
Sequence 40, Appl
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Sequence 16, Appl
Sequence 127, App
Sequence 139, App
Sequence 4, Appli
Sequence 4, Appli
Sequence 8, Appli
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US-09-191-724-6
US-09-818-009-10
US-09-799-78-16
US-09-799-978-16
US-10-649-852-40
US-10-649-852-40
US-09-853-386-127
US-09-853-386-127
US-09-853-386-127
US-09-853-386-128
US-10-242-822B-4
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US-10-649-852-8
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US-09-853-386-128
US-09-799-978-28
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Best Local Similarity 100.
Matches 444; Conservative
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           Sequence 15, Application US/09191724

Patent No. US20020055617A1

GRARRAL INFORMATION:

APPLICANT: Pertin, Marilyn H.

APPLICANT: Lewis, Kathy A.

APPLICANT: Lewis, Kathy A.

APPLICANT: Donald Grow, Cynthia W.

APPLICANT: Sawchenko, Paul

ITILE OF INVENTION: Cloning and Recombinant Production of TITLE OF INVENTION: Cloning and Recombinant Production of TITLE OF INVENTION: CRE Receptor(8)

FILE REFERENCE: Salk1748
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CURRENT PILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER APPLICATION NUMBER: US 08/374,009
EARLIER PILING DATE: 1995-01-17
EARLIER PILING DATE: 1994-12-09
EARLIER PILING DATE: 1994-12-09
EARLIER PILING DATE: 1993-05-25
EARLIER PILING DATE: 1993-06-23
EARLIER PILING DATE: 1993-06-23
EARLIER PILING DATE: 1993-06-18
EARLIER PILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FASEUSE FOR WINDOWN VERSION 3.0
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| Patent No. US2020049151A1
| GENERAL INFORMATION:
| APPLICANT: Murphy, Evelyn
| APPLICANT: Breenihan, Barry
| APPLICANT: Breenihan, Barry
| APPLICANT: Conneely, Orla
| TILLE OF INVENTION: Subfamily of Nuclear Transcription Factors
| TILLE OF INVENTION: Subfamily of Nuclear Transcription Factors
| TILLE OF INVENTION: WUMBER: US/09/853,386
| CURRENT FILING DATE: 2001-05-11
| PRIOR FILING DATE: 2000-05-12
| NUMBER OF SEQ ID NOS: 153
| SOFTWARE PATENTION NUMBER: US 60/203645
| PRIOR FILING DATE: 2000-05-12
| NUMBER OF SEQ ID NOS: 153
| SOFTWARE PATENTION NUMBER: US 60/203645
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100.0%; Score 2381; DB 3; Length 444;
Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0; Indels 0
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US-09-853-386-136
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US-09-853-386-136
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Sequence 708, Application US/10292798
Publication No. US20030235833A1
GENERAL INFORMATION:
APPLICANT: SUWA, MAKIKO
APPLICANT: ASAI, KIYOSHI
APPLICANT: ASI, KIYOSHI
APPLICANT: ABURATANI, HIROYUKI
APPLICANT: ABURATANI, HIROYUKI
TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS
FILE REFERENCE: 084335/166
CURRENT APPLICATION NUMBER: US/10/292,798
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 10/017,161
PRIOR FILING DATE: 2001-12-18
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CURRENT FILING DATE: 2003-08-26
PRIOR FILING DATE: 2003-08-26
PRIOR FILING DATE: BALLIER PLING DATE: 1998-11-12
PRIOR FILING DATE: BALLIER PLING DATE: 1998-11-12
PRIOR PLING DATE: BALLIER PLING DATE: 1998-11-7
PRIOR PLING DATE: EARLIER FILING DATE: 1995-01-17
PRIOR PLING DATE: EARLIER FILING DATE: 1994-12-09
PRIOR PLING DATE: EARLIER FILING DATE: 1994-12-09
PRIOR PLING DATE: EARLIER FILING DATE: 1993-05-25
PRIOR PLING DATE: EARLIER FILING DATE: 1993-06-25
PRIOR FILING DATE: EARLIER PILING DATE: 1993-06-25
PRIOR FILING DATE: EARLIER PILING DATE: 1993-06-28
PRIOR FILING DATE: EARLIER PILING DATE: 1993-06-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PASLER PILING DATE: 1993-06-18
SOFTWARE: PASLER PILING DATE: 1993-06-18
SOFTWARE: PASLER PILING DATE: 1993-06-18
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Best Local Similarity 100.0%; Pred. No. 1.7e-217;
Matches 444; Conservative 0; Mismatches 0;
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US-10-292-798-708
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                                                                                        APPLICANT: Slominski, Andrzej
TTTLE OF INVENTION: Variants of Corticotropin Releasing Hormone
TITLE OF INVENTION: Receptor Type 1 and Uses Thereof
FILE REFERENCE: D6420
CURRENT APPLICATION NUMBER: US/10/242,828
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 60/322,195
PRIOR APPLICATION NUMBER: US 60/322,195
NUMBER OF SEQ ID NOS: 49
SEQ ID NO 2
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| Publication No. US20040039173A1
| GENERAL INFORMATION:
| APPLICANT: Perrin, Marilyn H.
| APPLICANT: Chen, Ruoping | APPLICANT: Lewis, Kathy A.
| APPLICANT: Lewis, Kathy A.
| APPLICANT: Donaldson, Cynthia J.
| APPLICANT: Sawchenko, Paul | TITLE OF INVENTION: Cloning and Recombinant Production of TITLE OF INVENTION: CRF Receptor(8)
| TITLE OF INVENTION: CRF Receptor(8)
| FILE REPERENCE: Salk1748
| CURRENT APPLICATION NUMBER: US/10/649,193
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     Publication No. US20030113799A1
GENERAL INFORMATION:
APPLICANT: Pisarchik, Alexander
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US-10-649-193-15
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Sequence 2, Application US/09799978
Publication No. US20030165807A1
GENERAL INFORMATION:
PRICIANT: The Procter & Gamble Company
APPLICANT: Sheldon, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Regulating Muscle Mass or
TITLE OF INVENTION: Wethods for Identifying Compounds for Receptors
FILE REFERENCE: 8448
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                                                                                                                                                                                            Score 2186.5; DB 3; Length 415; Pred. No. 5e-199;
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Pred. No. 5e-199;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                          0; Indels
                                                                                                                                                                                                                                          0; Mismatches
       NUMBER OF SEQ ID NOS: 15
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/799,978 CURRENT FILING DATE: 2001-03-06
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Best Local Similarity 93.5%;
Matches 415; Conservative C
                                                                                                                                                                                         Query Match 91.8%;
Best Local Similarity 93.5%;
Matches 415; Conservative (
                                                                                                 TYPE: PRT
ORGANISM: Homo sapiens
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US-09-799-978-2
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                                                                           LENGTH: 415
                                                                                                                                             US-09-191-724-2
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US-09-799-978-2
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SEQ ID NO 2
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                                                                                                                                                                                                                                          Length 447;
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Sequence 2, Application US/09191724

Patent No. US20020055617A1

GENERAL INPORMATION:

APPLICANT: Perrin, Marilyn H.

APPLICANT: Lewis, Kathy A.

APPLICANT: Lewis, Kathy A.

APPLICANT: Donaldson, Cynthia J.

APPLICANT: Sawchenko, Paul

TILLE OF INVENTION: Cloning and Recombinant Production of
TILLE OF INVENTION: Cloning and Recombinant Production of
TILLE REFERENCE: Salk1748

CURRENT PILLING DATE: 1998-11-12

EARLIER APPLICATION NUMBER: US/09/191,724

CURRENT FILING DATE: 1998-11-17

EARLIER PILING DATE: 1993-01-17

EARLIER FILING DATE: 1993-05-25

EARLIER PILING DATE: 1993-05-25

EARLIER PILLING DATE: 1993-06-23

EARLIER PILLING DATE: 1993-06-23

EARLIER PILLING DATE: 1993-06-23

EARLIER PILLING DATE: 1993-06-18

EARLIER PILLING DATE: 1993-06-18
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                                                                                                                                                                                                                                          Score 2324; DB 4;
Pred. No. 4.6e-212;
                                                                                                                                                                                                                                                                                    1; Mismatches
PRIOR APPLICATION NUMBER: JP 2001-246789
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 2070
SOFTWARE: Patentin Ver. 2.1
SRQ ID NO 708
LENGTH: 447
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 99.8%;
Matches 433; Conservative
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US-10-292-798-708
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                                                                                            JUSTICATION OF US20040039173A1

Sequence 2, Application US/10649193

Publication No. US20040039173A1

JUBERRALL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Lewis, Kathy A.

APPLICANT: Lewis, Kathy A.

APPLICANT: Lewis, Kathy A.

APPLICANT: Lewis, Rathy A.

APPLICANT: Lewis, Rathy A.

APPLICANT: Sawchenko, Paul

TITLE OF INVENTION: CIDINING and Recombinant Production of

TITLE OF INVENTION: CRF Receptor (8)

TITLE OF INVENTION: CRF Receptor (8)

TITLE OF INVENTION: CRF Receptor (8)

FILE REFERENCE: Salk1748

CURRENT PELING DATE: 2003-06-26

PRIOR PELING DATE: BARLIER FILING DATE: 1998-10-17

PRIOR PELING DATE: EARLIER FILING DATE: 1995-01-17

PRIOR FILING DATE: EARLIER FILING DATE: 1995-01-17

PRIOR PELING DATE: EARLIER FILING DATE: 1993-01-17

PRIOR PELING DATE: EARLIER FILING DATE: 1993-06-25

PRIOR APPLICATION NUMBER: EARLIER PLING DATE: 1993-06-25

PRIOR PELING DATE: EARLIER FILING DATE: 1993-06-25

PRIOR PRIOR PELING DATE: EARLIER FILING DATE: 1993-06-18

NUMBER: OF SEQ ID NOS: 15

LENGTH: 415
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  392 ARAMSIPTSPTRVSFHSIKQSTAV 415
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                                                               RESULT 11
US-10-649-193-2
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Sequence 4, Application US/10649852
Publication No. US20040101911A1
GENERAL INFORMATION:
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert
APPLICANT: Select, Robert
TITLE OF INVENTION: Methods for Identifying Compounds for Receptors
TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors
                                                                                                                                                                                                                                   APPLICANT: The Procter & Gamble Company
APPLICANT: The Procter & Gamble Company
APPLICANT: Isfort, Robert
APPLICANT: Isfort, Russell
TITLE OF INVENTION: Methods for Identifying Compounds for Receptors
TITLE OF INVENTION: Using Corticotropin Releasing Factor Receptors
FILE REFERENCE: 8448R
CURRENT PELING DATE: 2003-08-27
FRIOR APPLICATION NUMBER: US 09/799,978
PRIOR APPLICATION WHERE: US 09/799,978
RIGH APPLICATION OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
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392 ARAMSIPTSPTRVSFHSIKQSTAV 415
                                                                                                                                                 Sequence 2, Application US/10649852
Publication No. US20040101911A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 415
                                                                                                                     US-10-649-852-2
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Sequence 483, Application US/09826509
; Sequence 483, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Liaw, Chen W.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G; TITLE OF INVENTION: Protein-Coupled Receptors
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT APPLICATION NUMBER: 60/195,747
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR APPLICATION NUMBER: 09/170,496
; RIGH APPLICATION NUMBER: 09/170,496
; RIGH APPLICATION NUMBER: 09/170,496
; RUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
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                                                                                                                  GQLVVRPCPAFFYGVRYNTTINNGYRECLANGSWAARVNYSBCQEILNEEKKSKVHYHVAV 120
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                      MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
                                                     1 MGGHPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPA
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                                                                                                                                                                                                                                                                                                                NI IHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
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                                                                                                                                                                                                                                                                121 IINYLGHCISLVALLVAFVLFLRL----
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Best Local Similarity
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; ORGANISM: Homc
US-09-826-509-483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NI IHWNLISAFILRNATWFVVQLTMSPBVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC
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                                                                                                                                                                                                                                                                                                                Score 2186.5; DB 4; Length 415;
Pred. No. 5e-199;
0; Mismatches 0; Indels 29;
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Pred. No. 5e-199;
0; Mismatches 0; Indels 29;
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US-10-450-097-14

Sequence 14, Application US/10450097

Publication No. US20040110252A1

GENERAL INFORMATION:

APPLICANT: Septegen Ltd

TITLE OF INVENTION: Yeast-Based Assay

FILE REFERENCE: DE/p701948FCT

CURRENT APPLICATION NUMBER: US/10/450,097

CURRENT APPLICATION NUMBER: GB 0030038.4

PRIOR APPLICATION NUMBER: GB 0030038.4

PRIOR FILING DATE: 2000-12-08

NUMBER OF SEQ ID NOS: 53

SOFTWARE: PatentIn Ver: 2.1

SEQ ID NO 14

LENGTH: 415

TYPE: PRT
                    CURRENT APPLICATION NUMBER: US/10/649,852
CURRENT FILLING DATE: 2003-08-27
PRIOR APPLICATION NUMBER: US 09/799,978
PRIOR FILING DATE: 2001-03-06
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin version 3.0
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Best Local Similarity 93.5%;
Matches 415; Conservative
                                                                                                                                                                                                                                                                                                                Query Match

91.8%;
Best Local Similarity 93.5%;
Matches 415; Conservative
                                                                                                                                                                                            ; LENGTH: 415
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-649-852-4
FILE REFERENCE: 8448R
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qa	121	IINYLGHCISLVALLVAFVLFLRLRSIRCLR 151	151
È	181	NITHWILISAFILENATWEVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWHGGGC 2	240
qq	152	NITHWNLISAFILENATWFVVQLTMSPEVHQSNVGWCRLVTAAYNYFHVTNFFWMFGEGC	211
È	241	YYDNEKCWPGKRPGVYTDYI	300
ପ୍ପ	212	YLHTAIVLTYSTDRLKKMMFICIGMGVPFPIIVAMAIGKLYYDNEKCWFGKRPGVTDYI	271
È	301	YQQPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVLLPLLGITYMLFF 3	360
q	272	YQGPMILVLLINFIFLFHIVRILMTKLRASTTSETIQYRKAVKAPLVLLPLLGITYMLFF	331
È	361	VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRMHRMQDKHSIRARV	420
QQ Q	332	VNPGEDEVSRVVFIYFNSFLESFQGFFVSVFYCFLNSEVRSAIRKRWHDKWDKHSIRARV 391	391
È	421	ARAMSIPTSPIRVSFHSIKQSTAV 444	
QQ	392	ARAMSIPTSPTRVSFHSIKQSTAV 415	

XI 300	YI 271
AWAIGKLYYDNEKCWFGKRPGVYTI	212 YLHTAIVLTYSTDRLRKMMFICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYI 271
TDRLRKWMFICIGWGVPFPIIVA	TDRLRKWMFICIGWGVPFPIIVA
241 YLHTAIVLTYST	212 YLHTAIVLTYST
	241 VLHTAIVLTYSTDRLRKWMFICIGMGVPFPIIVAMAIGKLYYDNEKCWFGKRPGVTDYI 300

Search completed: March 16, 2006, 17:24:47 Job time : 170 secs

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Sequence 43, Appl
Sequence 4164, Appl
Sequence 3164, Appl
Sequence 3106, Appl
Sequence 406, Appl
Sequence 4106, Appl
Sequence 7, Appli
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Sequence 2574, Appli
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Sequence 7537, Appli
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Sequence 4618, Appli
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Sequence 7537, Appli
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Sequence 17, Appl
                                                                        March 16, 2006, 17:22:09 ; Search time 22 Seconds (without alignments) 577.662 Million cell updates/sec
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1 MGGHPQLRLVKALLLLGLNP.....SIPTSPTRVSFHSIKQSTAV 444
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1: /cgn2_6/ptodata/2/pubpaa/USOB NEW PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USIO_NEW_PUB.pep:*
5.1.7
Biocceleration Ltd.
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US-11-090-439-29

US-11-10-597-31

US-11-127-877-43

US-10-131-826-306

US-10-973-1158-306

US-10-973-1158-306

US-10-973-1158-406

US-10-131-826-406

US-10-131-826-406

US-10-131-826-406

US-10-131-826-406

US-11-241-956-7

US-11-241-956-7

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US-10-055-877-177
US-11-174-819-17
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GenCore version
Copyright (c) 1993 - 2006
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26 93.5 3.9 432 7 US-11-087-099-167 Sequence 367, App 28 53.9 434 7 US-11-087-099-8116 Sequence 8116, Ap 28 92.5 3.9 358 7 US-11-174-816-52 Sequence 52, App 30 92.5 3.9 358 7 US-11-174-816-52 Sequence 24, App 31 92 3.9 337 7 US-11-174-816-43 Sequence 43, App 32 3.9 337 7 US-11-174-816-43 Sequence 43, App 32 3.9 489 7 US-11-087-099-9063 Sequence 211, App 34 91 3.8 358 7 US-11-087-099-9063 Sequence 88, App 34 7 US-11-087-099-9063 Sequence 68, App 35 30 489 7 US-11-074-816-68 Sequence 68, App 36 30 48 5 3.8 419 7 US-11-096-568A-25196 Sequence 25196, Ap 38 89.5 3.8 419 7 US-11-096-568A-25196 Sequence 25196, Ap 39 89.5 3.8 419 7 US-11-096-568A-25196 Sequence 59, App 37 424 7 US-11-096-568A-25196 Sequence 5196, App 40 89.5 3.8 410 7 US-11-096-568A-25195 Sequence 5196, App 41 88 5 3.7 412 7 US-11-01-64 Sequence 59, App 44 88 5 3.7 412 7 US-11-170-166-4 Sequence 4, App 11 45 88 5 3.7 412 7 US-11-170-166-4 Sequence 4, App 11 45 88 5 3.7 412 7 US-11-170-153-4 Sequence 4, App 11 45 88 5 3.7 412 7 US-11-170-153-4 Sequence 4, App 11 45 88 5 3.7 412 7 US-11-170-153-4 Sequence 4, App 11
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## ALIGNMENTS

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377 GTLRFIKLFTBLSFTSFQGLMVAILYCFVNNEVQLEFRKSWERWRLEHLHIQRDSSMKPL 436
                                          312 NFIFLFNIVRILMTKLRASTTSETIQYRKAVKATLVILPLLGITYMLF-FVNPGEDEVSR
                                                                                           371 VVFIYFNSFLE----SFQGFFVSVFYCFLNSEVRSAIRKRWHRW--QDKHSIRARVARAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 438
TYPE: PRT
ORGANISM: Homo sapiens
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US-11-090-439-29
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                                                                                                                                                                                                                                                            Sequence 3.10-201-411. Application US/10501411A
Publication No. US20060014678A1
GENERAL INPORMATION:
GENERAL INPORMATION:
APPLICANT: Come, Malcolm
APPLICANT: Come, Roger
APPLICANT: Bulter, Andrew
APPLICANT: Bloom, Stephen Robert
APPLICANT: Bloom, Stephen Robert
APPLICANT: Bloom, Stephen Robert
APPLICANT: Glatei, Modification of Feeding Behavior Using PYY and GLP-1
TITLE OF INVENTION: Modification of Feeding Behavior Using PYY and GLP-1
FILE REFERENCE: A 19248US
CURRENT APPLICATION NUMBER: US/10/501,411A
FRIOR FILING DATE: 2004-07-12
FRIOR FILING DATE: 2002-06-24
FRIOR FILING DATE: 2002-06-28
FRIOR FILING DATE: 2002-06-28
FRIOR FILING DATE: 2002-06-28
FRIOR FILING DATE: 2002-01-10
NUMBER OF SEQ ID NOS: 341
SOSTWARE: PATENTIN VENEROR 3.1
285 EK-CWFGKRPGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRAST----TSETIQYR 339
                    150 EGCCWLSNDTNSGFWWIIKGPILLIILVNFIFFINILRILVQKLRIDSLSPQTGETDQYR 209
                                                                        394
                                                                                         210 KKRLVKSTLLLLPLLGVTWILFLFAP-EDQSQGTLSLVFLYLFLILNSFQGFFVAVLYCF 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 --QWIFRLYVSIGWGVPLLFVVPWGIVKYLYEDEGCW-TRNSNMNYWLIIRLPILFAIGV 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99 -----YSECQEILNEEKKSKVHYHVAVIINY-LGHCISLVALLVAFVLFLRLRPGCTHW 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          152 GDQADGALEVGAPWSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTM---- 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               206 SPEVHQSNVGW------CRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTYSTDR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 LRKWMF---ICIGWGVPFPIIVAWAIGKLYYDNEKCWFGKRPGVYTDYIYQGPMILVLLI 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGGHP-QLRLVKALLLLGL-----NPVSASLQ------DQHCESLSLASN---I 39
                                                                     340 K -- AVKATLVLLPLLGITYMLFFVNPGEDE -- - VSRVVFIYFNSFLESFQGFFVSVFYCF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 SGLQCNASVDLIGTCWPRSPAGQLVVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVN-
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20.1%; Score 478; DB 6; Length 463;
Best Local Similarity 28.7%; Pred. No. 1.4e-36;
Matches 139; Conservative 74; Mismatches 172; Indels 100; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                            395 LNSEV 399
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LENGTH: 463
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64 VVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAVIIN 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            161 IHLNLFLSFILR-----AISVLVKDDVLYSSSGTLHCPDQPSSWVGCKLSLVFLQYCIMA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124 Y-LGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLRNI 182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 HPECRF------HLEIQEESTKCAELLRSQTEKHKACSGVWDNI-TCWRPANVGET
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Sequence 29, Application US/11090439
| Publication No. US20050266442A1
| GENERAL INFORMATION:
| APPLICANT: Squillace, Rachel
| APPLICANT: Weiner, Michael P.
| TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
| TITLE OF INVENTION: Anglomyolipoma Cell and Method of Use Thereof
| TITLE OF INVENTION: Anglomyolipoma Cell and Method of Use Thereof
| TITLE OF INVENTION: Anglomyolipoma Cell and Method of Use Thereof
| TITLE OF INVENTION: Anglomyolipoma Cell and Method of Use Thereof
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19.3%; Score 459.5; DB 7; Length 4
Best Local Similarity 28.2%; Pred. No. 6.8e-35;
Matches 118; Conservative 75; Mismatches 161; Indels
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US-11-090-439-31
Sequence 31, Application US/11090439
Publication No. US20050266442A1
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us-10-649-193-15.rapbn

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NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
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852 KLSALSSWKQTEKQNS 867
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                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
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Matches 89; Conserv
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                                                                                                                                                              US-11-206-587-17
                                                                                  LENGTH: 910
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Publication No. US20060040306A1

GENERAL INFORMATION:
GENERAL INFORMATION:
Teleby Kevin R.
APPLICANT: Leleby Kevin R.
TITLE OF INVENTION: 38650, 28472, 5495, 65507, 81588, AND
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: THEREOF
TITLE OF INVENTION: US/11/206,587
CURRENT APPLICATION NUMBER: US/11/206,587
CURRENT APPLICATION NUMBER: US/10/12,140
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR PILING DATE: 2000-11-08
PRIOR FILING DATE: 2000-11-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 VTVPCPKVPSNF-YSKAGNISKNCTSDGWSETFPDFVDACGYSDPEDESKITFYILVKAI 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               124 Y-LGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLRNI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 IHWNLISAFILRNATWFVVQLTMSPRVHQSNVG------W--CRLVTAAYNYFHVT 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161 IHLNLFLSFILR----AISVLVKDDVLYSSSGTLHCPDQPSSWVGCKLSLVFLQYCIMA 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 231 NPFWMFGEGCYLHTAIVLTYSTDRLRKWMFICIGWGVPPPIIVAWAIGKLYYDNEKCWFG 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 NPFWLLVEGLYLHTLLVAMLPPRRC-FLAYLLIGWGLPTVCIGAWTAARLYLEDTGGWDT 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             291 KRPGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRASTT--SETIQYRKAVKATLVL 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         275 NDHSV-PWWVIRIPILISIIVNPVLFISIIRILLQKLTSPDVGGNDQSQYKRLAKSTLLL 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64 VVRPCPAFFYGVRYNTTNNGYRECLANGSWAARVNYSECQEILNEEKKSKVHYHVAVIIN 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 HPECRF-----HLEIQEEBTKCTELLRSQTEKHKACSGVWDNI-TCWRPANVGET 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           334 IPLFGVHYMVPAVFP--ISISSKYQILFELCLGSFQGLVVAVLYCFLNSEVQCELKRKM 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 HPQLRLVKALLLLGLNPVSASLQDQHCESLSLASNISGLQCNASVDLIGTCWPRSPAGQL
                      APPLICANT: Squillace, Rachel
APPLICANT: Squillace, Rachel
APPLICANT: Weiner, Michael P.
TITLE OF INVENTION: Immortalized Human Tuberous Sclerosis Null
TITLE OF INVENTION: Anglomyolipoma Cell and Method of Use Thereof
FILE REPERENCE: 24118-502
CURRENT APPLICATION NUMBER: US/11/090,439
CURRENT PILING DATE: 2005-03-25
FRIOR APPLICATION NUMBER: 60/556,344
PRIOR FILING DATE: 2004-03-25
RIOR FILING DATE: 2004-03-25
SOFTWARE: PATENTING DATE: 2004-03-25
SOFTWARE: PATENTING DATE: 2004-03-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 19.3%; Score 459.5; DB 7; Length Best Local Similarity 28.2%; Pred. No. 6.8e-35; Matches 118; Conservative 75; Mismatches 161; Indels
                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
  GENERAL INFORMATION:
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yequence 43, Application Wo. US20050287565A1

yequence 43, Application No. Oscipation Special G.

yequence 43, Application No. Marcel

yequence 43, Application No. Marcel

yequence 43, Application No. Oscipation and Compound Assays For Inhibiting

yequence 43, Application No. Amyloid-Beta Protein Production

yequence 121 No. Oscipation No. No. 12

yequence 43, Application No. No. 12

yequence 43, Application No. No. 12

yequence 43, Application No. 12

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yequence 43, Application No. 12

yequence 43, Application No. 12

yequence 43, Application 3.3

yequence 43, Application 13.3

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              292 RPGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQ-----YRKAVKAT
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                                                                                                                                             Gaps
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2.7e-11;
Query Match
8.8%; Score 209; DB 7; Length 910
Best Local Similarity 23.4%; Pred. No. 2.7e-11;
Matches 74; Conservative 62; Mismatches 122; Indels
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APPLICANT: Stache-Crain, Birgit
APPLICANT: Stache-Crain, Burgit
APPLICANT: Stache-Crain, Susan
APPLICANT: Tang, Y. Ton
ITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt SEQ genes Version 1.0
SEQ ID NO 1164
LENGTH: 765
                                                                                                                                                                                                                 623 WKLTQKFSEINPDMKKLKKKARALTITAIAQLFLLGCTWVFGLFIF----DDRS-LVLTYV 677
481 P-----GSTIFLAGI- 508
                                 205 MSPEVHQSNVGW-CRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVLTYSTDRL-RKWMFIC 262
                                                                                                            263 IGWGVPPPII-VAWAI-GKLYYDNEKCWFGKRPGVYTDYIYQGPMILVLLIN-FIFLFNI 319
                                                                                                                                  320 VRILMIKLRASITSETIQYRKAVKATLVL-LPLLGITYM--LFFVNPGEDEVSRVVFIYF 376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 IGWGVPFPII-VAWAI-GKLYYDNEKCWFGKRPGVYTDYIYQGPMILVLLIN-FIFLFNI 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       320 VRILMTKLRASTISETIQYRKAVKATLVL-LPLLGITYM--LFFVNPGEDEVSRVVFIYF 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 PGCTHWGDQADGALEVGAPWSGAPFQVRRSIRCLRNIIHWNL-ISAFILRNATWFVVQLT 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      532 ---ENEGGOVGLRCRLVAGILHYCFLAAFCWMSLEGLELYFLVVRVFOGGGLSTRWLCL- 587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ||| : :: || : : || 450 NGSTTCQCSHLSSFAIL-----MAHYDVEDWKLTLITRVGLALSLFCLLCILTFLLVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      509 ---ENEGGQVGLRCRLVAGLLHYCPLAAFCWMSLEGLELYPLVVRVFQGQGLSTRWLCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match

8.7%; Score 207.5; DB 6; Length 765;
Best Local Similarity 26.9%; Pred. No. 3.1e-11;
Matches 89; Conservative 51; Mismatches 128; Indels 63
                                                                                                                                                                                                                                                                 377 NSFLESFOGFFVSVFYCFLNSEVRSAIRKRW 407
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1164, Application US/10821234 Publication No. US20050255114A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                -10-821-234-1164
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US-10-131-826A-306
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE SERENGE: P3330R1C128
CURRENT PELICATION NUMBER: US/10/131,826A
CURRENT PELING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: 60/05991
PRIOR PELING DATE: 1997-06-18
PRIOR PELING DATE: 1997-06-17
PRIOR PELING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---YHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALE
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8.64; Score 205; DB 6; L
Best Local Similarity 23.24; Pred. No. 4.7e-11;
Matches 86; Conservative 54; Mismatches 135;
Sequence 306, Application US/10131826A Publication No. US20050245730A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smith, Victoria
Stewart, Timothy A.
                                                                                                                                                                                                                Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Qiang
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Wood, William
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                                                                                                          APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
                                                                                                                                                                                                                                                                                                                                                           Goddard, Audrey
Godowski, Paul J.
Gurney, Austin L.
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494 AGLIHYFFIDAFAMMCIEGIHLYLIVVGVIYNKGFLHKNFYI---FGYLSPAVVVGFSAA 550
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                                                                                                                                                                                                                                                                                                                    336 IQY----RKAVKATLVLLPLLGITY---MLFFVNPGEDEVSRVVFIYFNSFLESFQGFFVS 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    608 SCFENIRSCARGALALLFLLGTTWIPGVLHVVH-----ASVVTAYLFTVSNAFOGMFIF 661
161 VGAPWSGAPFQVRRSIRCLRNIIHWNLISAFILRNATWFVVQLTMSPEVHQSNVGWCRLV 220
                                                           450 ----WFFS------BIQSTRITIHKNLCCSLFLABLVFLVGINT-----NTWKLFCSII 493
                                                                                                                                     221 TAAYNYFHVTNFFWMFGEGCYLHTAIV-LTYSTDRLRKWMFICIGWGVPFPIIV---AWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GRENEAL INFORMATION:
GRENEAL INFORMATION:
GRENEAL INCYTE GENOMICS INC.; BAUGHN, Mariah R.;
APPLICANT: GRAUL Richard C.; CHAMIA, Narinder K.;
APPLICANT: GRAUL Richard C.; CHAMIA, Narinder K.;
APPLICANT: RANKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;
APPLICANT: THORNYON, Michael B.; KALLICK, Deborah A.;
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: WE, Henry; LU, Yan;
APPLICANT: WE, Henry; LU, Yan;
APPLICANT: WE, Henry; LU, Yan;
APPLICANT: MUREND, Neil; KHAN, Farrah A.;
APPLICANT: MUREND, Danniel B.; EEB, Ernestine A.;
APPLICANT: MUREND, Danniel B.; EEB, Ernestine A.;
APPLICANT: MUREND, Danniel B.; EEB, Ernestine A.;
APPLICANT: MUREND, Danniel B.; LEB, Ernestine A.;
APPLICANT: MUREND, Danniel B.; LEB, Ernestine A.;
APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
TITLE REFERENCE: PL-0236 USN
CURRENT APPLICATION NUMBER: US/11/241,956
CURRENT APPLICATION NUMBER: US 60/245,855
FRIOR APPLICATION NUMBER: US 60/242,322
PRIOR APPLICATION NUMBER: US 60/242,322
PRIOR APPLICATION NUMBER: US 60/242,323
PRIOR APPLICATION NUMBER: US 60/245,943
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
PRIOR FILING DATE: 2000-11-03
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US-11-241-956-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/11241956 Publication No. US20060024792A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      390 VFYCFLNSEVR 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  662 LFLCVLSRKIQ 672
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ORGANISM: Homo sapiens
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APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin I.
FITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17;
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                                                                                                                                                                                      336 IQY---RKAVKATLVLLPLLGITY---MLFFVNPGEDEVSRVVFIYFNSFLBSFQGFFVS 389
   277 IGKLYYDNEK-CWFGKRPGVYTDYIYQGPMILVLLINFIFLFNIVRIIMTKLRASTTSET 335
                                            73 YGVRYNTTNNGYRECLA-----KUGSWAA---RVNYSECQEILNEEKKS----KVH
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Best Local Similarity 23.2%; Pred. No. 4.7e-11;
Matches 86; Conservative 54; Mismatches 135; Indels 96; Gaps
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PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-19
PRIOR PELING DATE: 2001-12-01
PRIOR PELING DATE: 2000-12-01
PRIOR PELING DATE: 2000-06-16
PRIOR PELING DATE: 2000-06-16
PRIOR PELING DATE: 2000-06-16
PRIOR PELING DATE: 2000-03-02
PRIOR PELING DATE: 1999-05-25
PRIOR APPLICATION NUMBER: US 60/135,736
PRIOR APPLICATION NUMBER: US 60/135,736
PRIOR PELING DATE: 1999-05-25
PRIOR PELING DATE: 1999-05-05-16
PRIOR PELING DATE: 1999-05-05-16
PRIOR PELING DATE: 1999-05-05-16
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PRIOR PELING DATE: 1999-03-05
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CURRENT APPLICATION NUMBER: US/10/973,115B
CURRENT FILING DATE: 2004-10-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 10/145,747
PRIOR FILING DATE: 2002-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 306, Application US/10973115B
Publication No. US20060040351A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E.
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Stewart, Timothy A.
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Gurney, Austin L
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662 LFLCVLSRKIQ 672
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US-10-973-115B-306
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                                                                                                                                                                      97 VNYSECQEILNEEKKSKVHYHVAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQAD 156
                                                                                                                                                                                                                                                            157 GALEVGAPWSGAPPQ-VRRSIR------CLRNIHWNLISAFILRNATWFVVQLT 204
                                                                                                                                                                                                                                                                                                                                               205 MS-------PEVHQSNV--GWCRLVTAAYNYFHVTNFFWMFGEGCYLHTAIVL 248
                                                                                                                                                                                                                                                                                                                                                                                                                                       249 TYSTDRLRKWMFI-CIGWGVPFPIIVAWAIGKLY------YDNEK-CWFG---- 290
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360 SASVDMVFSPKYNQKBFQLYSYACVYWNLSAKDWDTYGCQKDKGTDGFLRC-----R
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APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Wood, William
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3330R1C128
                                                                                   45 NASVDLIGTCWPRSPAGQLVVRPCPAF-----FYGVRYNTTNNGYRECLANGSWAAR
Query Match
8.0%; Score 189.5; DB 7; Length 797;
Best Local Similarity 20.7%; Pred. No. 1.5e-09;
Matches 96; Conservative 79; Mismatches 165; Indels 123; Gaps
                                                                                                                                                                                                                 412 CNHTTNFAVLMTFKKDYQYPKSLDILSNVGCALSVTGLALTVI------
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CURRENT FILING DATE: 2002-04-24
PRIOR PELING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-06-18
PRIOR PILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059113
PRIOR PILING DATE: 1997-09-17
PRIOR PRING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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Filvaroff, Ellen
Gao, Wei-Qiang
Gerritsen, Mary E.
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Stewart, Timothy A.
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Godowski, Paul J.
Gurney, Austin L.
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Best Local Similarity 22.6%; Pred. No. 6.4e-09;
Matches 83; Conservative 46; Mismatches 122; Indels 116; Gaps
PRIOR FILING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR PLING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR APPLICATION NUMBER: 60/059263
PRIOR APPLICATION NUMBER: 60/059263
PRIOR PPLING DATE: 1997-09-19
PRIOR PPLING DATE: 1997-09-19
PRIOR PPLING DATE: 1997-09-19
PRIOR PPLING DATE: 1997-09-19
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Tumas, Daniel
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Filvaroff, Ellen
Gao, Wei-Quiang
Gerritsen, Mary E
Goddard, Audrey
Godowski, Paul
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APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
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Smith, Victoria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo Sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 FLNSEVR 400
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348 FLLCAPTWMGLEAFHLYLLAVRVFNTYFGHYFLKLSLVGWGLPALMVIGTGSANSYGLYT 407
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APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
APPLICANT: UGUYEN, Danniel B.; LEB, Ernestine A.;
APPLICANT: LU, DYUNG Alina M.; LSGN, Craig H.;
APPLICANT: LU, DYUNG Alina M.; LSGN, Craig H.;
APPLICANT: LU, DYUNG ALINA M.; LSGN, Craig H.;
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REPERROR: P1-0256 USN
CURRENT APPLICATION NUMBER: US/11/241,956
CURRENT FILING DATE: 2005-10-04
FRIOR PELLING DATE: 2001-03-28
PRIOR PELLING DATE: 2001-03-28
PRIOR PELLING DATE: 2001-03-28
PRIOR PELLING DATE: 2000-11-03
PRIOR PELLING DATE: 2000-11-03
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NAME/KEY: misc feature
COTHER OF 1 Incyte ID No: 55012817CD1
US-11-241-956-7
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Best Local Similarity 23.8*
Matches 72; Conservative
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ORGANISM: Homo sapiens
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US-11-200-822-3
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODIN
TITLE OF INVENTION: SAME
FILE REFERENCE: 39870-3330R1C300C1
CURRENT PLING DATE: 2004-10-23
CURRENT FILING DATE: 2004-10-23
PRIOR FILING DATE: 2002-05-14
PRIOR PILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: WS 10/028,072
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-12-01
PRIOR PILING DATE: 2000-05-16
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 2000-03-02
PRIOR PILING DATE: 1999-03-05
PRIOR FILING DATE: 1999-03-05
NUMBER: WS SEQ ID NOS: 550
LENGTH: 693
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APPLICANT: GRAUL Richard C.; CHAWLA, Narinder K.;
APPLICANT: GANDHI, Ameena R.; HAFRLIA, April J.A.;
APPLICANT: RAMKUMAR, Jayalaxmi; TRIBOULEY, Catherine M.;
APPLICANT: TAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: YAO, Monique G.; ELLIOTT, Vicki S.;
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             509 GTYVPGYLLK--LSAMGWG--PPIFLVTLVALVDVDN----
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Publication No. US20060024792A1
GENERAL INFORMATION:
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Matches 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2470 BVRDVNTGPMR--FYYMLGMGVP-AFITGLAVGLDPBGYGNPDFCWL----SIYDTLIMS 2522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247 -VLTYSTDRLRKWMFICIGWGVPFPIIVAWAIG---KLYYDNEKCWFGKRPGVYTDYI-- 300
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                  TITLE OF INVENTION: Methods of Classifying, Diagnosing, Stratifying and TITLE OF INVENTION: Treating Cancer Patients and Their Tumors FILE REPERBURE: 20028350-0049
CURRENT APPLICATION NUMBER: US/11/200,822
CURRENT PILING DATE: 2005-08-10
NUMBER OF SEQ ID NOS: 15
SQCID NO 3
ERGGID NO 3
ERGGID NO 3
ERGGID NO 3
ERGGID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
6.9%; Score 165; DB 7; Length 2923;
Best Local Similarity 22.3%; Pred. No. 1.3e-06;
Matches 78; Conservative 64; Mismatches 113; Indels 94; Gaps
                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cadherin EGF
OTHER INFORMATION: LAG Seven Pass G-Type Receptor 2
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APPLICANT: GRAUL Richard C.; CHAMIA, Warinder K.;
APPLICANT: GANDHI, Ameena R.; HAFALIA, April J.A.;
APPLICANT: THORNOM, Machael B.; FALLICK, Deborah M.;
APPLICANT: THORNOM, Michael B.; FALLICK, Deborah A.;
APPLICANT: YAO, Monique G.; ELLIOTT, VICKI S.;
APPLICANT: BURFORD, Neil; KHAN, Farrah A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: YUE, Henry, LU, Yan;
APPLICANT: ARVIZU, Chandra S.; ROOPA, Reddy M.;
APPLICANT: NGUYEN, Danniel B.; LEE, Ernestine A.;
APPLICANT: LU, Dyung Aina M.; ISON, Craig H.;
APPLICANT: WALSH, Roderick T.; POLICKY, Jennifer L.
TILLE OF INVENTION: G-PROTEIN COUPLED RECEPTORS
FILE REFERENCE: PI-0236 USN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/241,956
CURRENT FILING DATE: 2005-10-04
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PRIOR FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30661
PRIOR PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: US 60/245,855
PRIOR FILING DATE: 2000-11-03
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Publication No. US20060024792A1
GENERAL INFORMATION:
APPLICANT: Bostein, et al
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315 ILTYITYVGLGISICSLILCL------SIEV-LVWS----QVTKTEI 350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 288 WFG-KRPGVYTDYIYQGPMILVLLINFIFLFNIVRILMTKLRASTTSETIQYRKAV---- 342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         118 VAVIINYLGHCISLVALLVAFVLFLRLRPGCTHWGDQADGALEVGAPWSGAPFQVRRS-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            343 KATLVLLPLLGITYMLFFVNPGEDEVSRVVFIYFNSFLESFQ 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 7477708CD1
US-11-241-956-2
PRIOR APPLICATION NUMBER: US 60/242,322
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-32
PRIOR PLLING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 60/249,343
PRIOR APPLICATION NUMBER: US 60/247,587
PRIOR PILING DATE: 2000-11-09
PRIOR FILING DATE: 2000-11-09
PRIOR PILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: US 60/245,900
PRIOR PILING DATE: 2000-11-03
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PERL PROGRAM
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US-10-649-193-14 1582

1 cgagcccgcagccgcccgcc......gctctccccctgcagccgtg 1582 Title: Perfect score: Sequence:

Scoring table:

Total number of hits satisfying chosen parameters:

4996997 segs, 3332346308 residues IDBNTITY NUC Gapop 10.0 , Gapext 1.0 Searched:

9993994

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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genesequi200s:\*
genesequi200s:\*
genesequi2001bs:\*
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genesequi2002as:\*
genesequi2003as:\* geneseqn2003cs:\* N Geneseq 21:\* 1: geneseqn198 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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п	1582	100.0	1582	9	AAD44489	Aad44489 Human CRF
7	1582	100.0	1582	ω	ABX93041	Abx93041 Human cor
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4	1582	100.0	1582	12	ADJ65809	Adj65809 Human cor
S	1398	88.4	1495	N	AAQ81952	Aag81952 Human pit
9	1398	88.4	1495	0	AAT28968	Aat28968 Human CRF
7	1398	88.4	1495	ø	AAD44482	Aad44482 Human CRF
80	1398	88.4	1495	æ	ABX93034	Abx93034 Human cor
6	1398	88.4	1495	0	ABX11833	Abx11833 Human cDN
10	1398	88.4	1495	17	ADJ65796	Adj65796 Human cor
c 11	1398	88.4	2579	9	AAS62243	Aas62243 cDNA sequ
12	1396.4	88.3	2536	12	AD029851	Ado29851 Human GPC
13	1396.4	88.3	2536	12	AD050782	Ado50782 Human cor
14	1335	84.4	1335	2	ACA56762	Aca56762 Human sig
15	1335	84.4	1335	12	AD156558	Adis6558 Human pol
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17	1188	75.1	1285	12	ADO50784	Ado50784 Human cor
18	1167.4	73.8	1278	~	AAT37068	Aat37068 Human cor
19	1154.2	73.0	10042	9	ABK95585	Abk95585 Yeast rep

Lewis KA, Vale WW, Donaldson CJ, Sawchenko P;

Perrin MH, Chen R,

Abk95583 DNA encod Adv2663 Human psy Abi97981 Non-endog Abk51690 Human CRF Adv36798 Human cor Adv36788 Human cor Adv36788 Rat corti Aav36978 Rat Corti Abx11835 Rat corti Abx11835 Rat corti Abx11835 Rat corti Abx11835 Rat corti Adv365800 Rat corti Adv365800 Rat corti Adv365800 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti Adv36590 Rat corti	Ado50820 Cow corti Ad49981 Murine co Ado50802 mouse cor Ad49984 Ovine cor Ado50808 Sheep cor Ado30142 Mouse GPC Ad19973 Human cor Ado50786 Human cor Ado50786 Human cor Ad19991 Chicken c
<b>4 444 44444 44</b>	12 ADOS0820 6 AAL49981 6 AAL49984 12 ADOS0808 12 ADOS0808 12 ADOS0142 6 AAL49973 8 ABZ47795 12 ADOS0786 6 AAL49991
12248 12248 12248 12206 12206 14411 14411 14411 12411 12411 12411	1248 2273 2273 1248 1248 1248 1146 1146
6 6 6 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	641 63.6 63.6 63.5 63.5 63.5 7.2 7.2
1151 1151 1151 1057 1057 1057 1057 1035.2 1035.2 1035.2 1035.2 1035.2	1013.4 1006.8 1003.8 1003.8 973.4 919 919 919
01000000000000000000000000000000000000	. W W W W A A A A A A A A A A A A A A A

## ALIGNMENTS

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Human, G protein-coupled corticotropin-releasing factor receptor; CRF; CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy; Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa; receptor; alcoholism; CRF-RA2; gene; ss.
                                                                                                                                            Location/Qualifiers
82. 1416
**tag= a
/product= "hCRF-RA2 splice variant protein"
                                                            Human CRF-RA2 splice variant cDNA
       AAD44489 standard; cDNA; 1582 BP.
                                                                                                                                                                                                                                             93US-00079320.
93US-00110286.
94WO-US005908.
94US-00353537.
95US-00483139.
                                                                                                                                                                                                                           98US-00191724.
                                           (first entry)
                                                                                                                                                                                                                                                                                                           CHEN R.
LEWIS K A.
VALE W W.
DONALDSON C J.
                                                                                                                                                                                                                                                                                                   PERRIN M H.
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23-AUG-1993;
25-MAY-1994;
09-DEC-1994;
07-JUN-1995;
                                          13-DEC-2002
                                                                                                                             Homo sapiens
                                                                                                                                                                                                                            12-NOV-1998;
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                          AAD44489;
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                                                                                                                                                                                                                          The invention relates to recombinant mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having high affinity for CRF and nucleic acid molecules encoding such receptor proteins. Polypeptides of the invention can be used to reduce high levels of adrenocorticotrophic hormone caused by excess CRF and so can be used to treat diseases such as Cushing's syndrome, pituitary tumours, chronic stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They are used in pharmaceuticals and in the production of antibodies. The present sequence is human CRF-RA2 splice variant cDNA
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                                                                             New isolated recombinant mammalian G protein-coupled corticotropin-
releasing factor receptor protein for treating e.g. Cushing's syndrome,
pituitary tumors, stress, anorexia, alcoholism or irritable bowel
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100.0%; Pred. No. 0;
live 0; Mismatches
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Matches 1582; Conservative C
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P-PSDB; AAE26685.
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Human; gene; 88; corticotropin-releasing factor receptor; CRP; G procein-coupled corticotropin-releasing factor receptor; Drocein-coupled corticotropin-releasing factor receptor; phypothalamic peptide; pituitary adrenocorticotrophic hormone; ACTH; adrenal glucocorticoid; gene therapy; cortisol; Alzheimer's disease; Cushing's disease; anorexia nervosa; alcoholism; antiinflammatory; irritable bowel syndrome; melancholic depression; neuroprotective; nootropic; antidepressant; splice variant.
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wew nucleic acid and its encoded G protein-coupled corticotropin-releasing factor receptor, useful for diagnosing or treating e.g. ACTH levels or high cortisol levels associated with Alzheimer's disease or Cushing's disease.

Disclosure; Col 57-62; 42pp; English.

The invention discloses an isolated nucleic acid, which encodes a mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein. CRF is a hypothalamic peptide which stimulates the secretion and biosynthesis of pitultary adrenocorticotropinc hormone (ACTH) leading to increased adrenal glucocorticotropinc hormone (ACTH) leading to increased adrenal glucocorticotd production. The nucleic acid, or the CRF receptor that it encodes, is useful in bioassays. The nucleic acid or CRF receptor is particularly useful for providing recombinant receptors that allows the development of less expensive, more sensitive and automated means for assaying CRF and CRF-like compounds and developing CRF-based cherapeutics. The nucleic acid, or fragments of its encoded receptor, are useful in therapy, e.g. gene therapy for reducing ACTH levels or treating high cortisol levels associated with Alzheimer's diseases, Cushing's are also useful in diagnostic assays, e.g. for diagnosing Alzheimer's caseases are alcoholism. The sequence presented is the human splice variant of CRF-RI, CRF-R2, CDNA

1021 1081 셤 용 ઠ ð ò ઠે ö 120 120 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCCTCCAGGACCAGCACTGCGAGAGCCTG 180 9 9 CGAGCCCGCAGCCGCCCGCCGGTTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC 1 CGAGCCCGCAGCCCCCCCCCCGGTTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC 61 GGTAGCCGAGCGAGCGAGGATGGGAGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTT 61 derageceaagecegageargegagegeaccegeagerecerereargagecerr Gaps ö DB 8; Length 1582; Sequence 1582 BP; 286 A; 518 C; 437 G; 341 T; 0 U; 0 Other; Indels ö s; Score 1582; I s; Pred. No. 0; 0; Mismatches 100.08; Best\_Local Similarity 100.0%; Matches 1582; Conservative ( -Query Match 셤 셤 à ઠે ò

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                       1321 CACTCGATCCGTGCCCGAGTGGCCCGTGCCATGTCCATCCCCACCTCCCCAACCCGTGTC 1380
                                                                                           1501 GACCTGTTAGGTCTCATGCCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGG 1560
                                                                                                                                                          1201 ATCTACTTCAACTCCTTCCTGGAATCCTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGT 1260
                                                                                                                 Human; ss; gene; corticotropin releasing factor receptor; hCRP-RAl; Cushing's disease; pituitary tumour; Alzheimer's disease; melancholic depression; anorexia nervosa; chronic stress; alcoholism; hypercortisolaemia; gastrointestinal disorder; irritable bowel syndrome; pre-eclampsia; pregnancy-induced complication; arthritis; abortion;
                                                                                AGCITICACAGCATCAAGCAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCCC
                                               CACTCGATCCGTGCCCGAGTGGCCCGTGCCATCTCCCCACCTCCCCAACCCGTGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel cell line expressing nucleic acid expression vector comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Donaldson CJ,
                                                                                                                                                                                                                                                                                                                                                                                                           /product= "hCRF-RA1 splce variant"
                                                                                                                                                                                                                                                                                           Human cDNA encoding hCRF-RA1, splice variant.
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94WO-US005908.
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95US-00483139.
98US-00191724.
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P-PSDB; ABG76402.
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07-JUN-1995;
12-NOV-1998;
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25-MAY-1994;
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The invention relates to a cell line expressing a recombinant corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid expression vector.

Corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid expression vector.

Compounds a recombinant CRP-R. The vector encodes human CRF-R, subtype A, receptor in a suitable host cell, by expressing the vector, where the nucleic acid encodes CRF-R that binds GRP or nucleic acid degenerate to the naturally occurring nucleic acid. The cell line is useful for expressing hortern by recombinant techniques and in binding assays using CRF-R which are used for rapidly screening large number of compounds to determine which compounds are capable of binding to CRF-R, and for identifying new CRF-like ligands. The polypeptides expressed by the cell line inhibit CRF binding to CRP-R and can inhibit CRF-in undeed adrenocorticotropin hormone (ACTH) release in vitro by several cells, and so are useful for radding high ACTH levels caused by excess CRF, and for treating Cushing's disease, pitulary tumours, alzaheimer's disease, creating Cushing's disease, pitulary tumours, alzaheimer's disease.

CC melancholic depression, anorexia nervosa, chronic stress, alcoholism and hyporecortisolaemia. The proteins are also useful for treating gastrointestinal disorders such as irritable bowel syndrome, abnormalities such as pre-eclampsia, which occur during pregnancy, to creduce pregnancy-rinduced compilcations and increased CRF lavels which can ocherwise result in excessive release of ACTH. The proteins are also checker pregnancy-ried and areas as the disoness and increased CRF lavels and ocher domesticated animals, inducing twinning in livestock and other domesticated animals, inducing twinning in livestock and other domesticated animals, inducing temperation in livestock and other domesticated animals, inducing temperature asplication of the receptor, human corticotropin releasing factor receptor, hCRF-RADI ceptor receptor, hCRF-RADI ceptor receptor and other domestic
nucleic acid encoding human corticotropin releasing factor (CRF) receptor useful for reducing high adrenocorticotropin hormone, by binding to CRF.
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ative 0; Mismatches
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The invention relates to an isolated mammalian G protein-coupled corticotropin-releasing factor (CRP) receptor protein or polypeptide from Rat, Mounes or human appearing as ADJ65801, ADJ65805, or ADJ65810, encoded by the nucleic acids appearing as ADJ65800, ADJ65802, ADJ65804, or ADJ65809. Also included are a composition comprising CRF-R, an antibody generated against CRF-R and a diagnostic, kit, for assaying of or the presence in biological fluids of CRF-R protein, protein analogues and/or fragments, comprising CRF-R) and/or one or more antibodies. The protein, polynucleotide or composition is useful in diagnosing and treating Alzheimer's disease, melancholic depression, anorexia nervosa, Cushing's disease, hypercortisolaemia or alcoholism, gastrointestinal disorders (e.g. irritable bowel syndrome) or physiological conditions (e.g. inflammation or Addison's disease), in regulating cardiac perfusion and in modulating blood pressure, thus combat hypotension. The present sequence encodes human splice variant CRF-RAZ.
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New mammalian G protein-coupled corticotropin-releasing factor receptor protein, useful in diagnosing and treating Alzheimer's disease, anorexia nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
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                                                                                                                           Human corticotropin-releasing factor receptor CRF-RA2 cDNA
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                                                                                                                                                                                                                                                                   The protein encoded by this sequence can be used to determine CRF (e.g. over- or under-production, high levels of CRF late in pregancy may indicate risk of premature labor). Cells expressing the protein are used to identify e.g. antibodies, which can be used to modulate signal transduction activity mediated by CRF receptors. Typical applications are in the treatment of Cushing's disease, pituitary tumors, etc. (Updated on 25-MAR-2003 to correct PN field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated corticotropin-releasing factor receptor (CRF-R) - used to develop prods. for modulating signal transduction activity mediated by CRF-R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACC
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P-PSDB; AAR97290.
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The invention relates to recombinant mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor (CRF-R) proteins having high affinity for CRF and nucleic acid molecules encoding such receptor proteins. Polypeptides of the invention can be used to reduce high levels of adrenocorticotrophic hormone caused by excess CRF and so can be used to treat diseases such as Cushing's syndrome, pituitary tumours, chronic stress, anorexia nervosa, alcoholism and irritable bowel syndrome. They are used in pharmaceuticals and in the production of antibodies. The present sequence is human CRF-RA1 cDNA
                                                                                                                                                                           Human; G protein-coupled corticotropin-releasing factor receptor; CRF; CRF-R; adrenocorticotrophic hormone; irritable bowel syndrome; therapy; Cushing's syndrome; pituitary tumour; chronic stress; anorexia nervosa; receptor; alcoholism; CRF-RA1; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               releasing factor receptor protein for treating e.g. Cushing's syndrome, pituitary tumors, stress, anorexia, alcoholism or irritable bowel
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Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;

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The invention discloses an isolated nucleic acid, which encodes a mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein. CRF is a hypothalamanic peptide which stimulates the secretion and blosynthesis of pituitary adrenocorticotrophic hormone (ACTH) leading to increased adrenal glucocorticotid production. The nucleic acid, or the CRF receptor is particularly useful in bioassays. The nucleic acid or CRF receptor is particularly useful in bioassays. The nucleic acid or CRF receptor is particularly useful for providing recombinant receptors that allows the development of less expensive, more senaltive and automated means for assaying CRF and CRF-like compounds and developing CRF-based therapy e.g. gene therapy for reducing ACTH levels or treating high cortisol levels associated with Alzheimer's diseases, Cushing's diseases, molecula in diagnostic assays, e.g. for diagnosting Alzheimer's diseases or are also useful in diagnostic assays, e.g. for diagnosting Alzheimer's diseases or alcoholism. The sequence presented is the human CRF-RI CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGCCCGCGTGAATTACTCCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAGCAAG 420
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                                                                                                                                                                                                              New nucleic acid and its encoded G protein-coupled corticotropin-
releasing factor receptor, useful for diagnosing or treating e.g. ACTH
levels or high cortisol levels associated with Alzhelmer's disease or
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                                                                                                                     Sawchenko
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Pred. No. 0;
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                                                                                                                   Donaldson CJ,
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93US-00110286.
94WO-US005908.
94US-00353537.
                                                                           (SALK ) SALK INST BIOLOGICAL
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Best Local Similarity 94.5%;
Matches 1495; Conservative
                                                                                                                                                        WPI; 2003-327461/31.
                                                                                                                                                                                                                                                                         Cushing's disease.
                                                                                                                                                                            P-PSDB; ABU08075
                    25-MAY-1994;
09-DEC-1994;
                                                                                                                   Perrin MH,
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                                                                             GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCTGCCCCCCTCCTGGGC
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The invention relates to a cell line expressing a recombinant corticotropin releasing factor receptor (CRF-R) encoded by a nucleic acid expression vector, or a cell line containing a nucleic acid vector encoding a recombinant CRF-R. The vector encodes human CRF-R, subtype A, variant 1 (hCRF-RA1). Also included is expressing a recombinant CRF ceeptor in a suitable host cell, by expressing the vector, where the nucleic acid encodes CRR-R that binds CRF or nucleic acid degenerate to the naturally occurring nucleic acid. The cell line is useful for expressing hCRF-RA1 protein by recombinant techniques and in binding assays using CRF-R which are used for rapidly screening large number of compounds to determine which compounds are capable of binding to CRF-R, and for identifying new CRF-like ligands. The polypeptides expressed by the cell line inhibit CRF binding to CRF-R and can inhibit CRF-induced afrencorticotropin hormone (ACTH) release in vitro by several cells, and care useful for reducing hAgh ACTH levels caused by excess (RRF, and for treating Cushing's disease, pituitary tumours, Alzheimer's disease, melancholic depression, anorexia nervosa chronic stress, alcoholism and hypercortisolaemia. The proteins are also useful for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel cell line expressing nucleic acid expression vector comprising nucleic acid encoding human corticotropin releasing factor (CRF) receptor useful for reducing high adrenocorticotropin hormone, by binding to CRF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cushing's disease; pituitary tumour; Alzheimer's disease; melancholic depression; anorexia nervosa; chronic stress; alcoholism; hypercortisolaemia; gastrointestinal disorder; irritable bowel syndrome; pre-eclampsia; pregnancy-induced complication; arthritis; abortion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human cDNA encoding corticotropin releasing factor receptor, hCRF-RAI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene; corticotropin releasing factor receptor; hCRF-RA1;
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/product= "hCRF-RA1"
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93US-00110286.
94WO-US005908.
94US-00353537.
95US-00374009.
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P-PSDB; ABG76046.
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25-MAY-1994;
09-DEC-1994;
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abnormalities such as pre-eclampsia, which occur during pregnancy, to treduce pregnancy-induced complications and increased CRF levels which contentwise result in excessive release of ACTH. The proteins are also useful for locally treating arthritis and other similar aliments, modulating action of CRF in mammals, treating the pregnancy-related pathological disorders in mammals. The CRF-R polypeptides are used in such areas as the diagnosis and/or treatment of CRF-dependent tumours, enhancing the survival of brain neurons, inducing abortion in livestock and other domesticated animals, inducing twinning in livestock and other domesticated animals. The present sequence encodes corticotropin
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                                                                                                                                                                                                                                                                                              87;
                                                                                                                                                                                                                                                         Query Match

88.4%; Score 1398; DB 9; Length 1495;
Best Local Similarity 94.5%; Pred. No. 0;
Matches 1495; Conservative 0; Mismatches 0; Indels 87
                                                                                                                                                                                                                          Sequence 1495 BP; 271 A; 496 C; 403 G; 325 T; 0 U; 0 Other;
                                                                                                                                                                                          releasing factor receptor, hCRF-RA1
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361 GCCGCCCGCGTGAATTACTCCGAGTGCCAGGAGATCCTCAATGAGGAAAAAAGCAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated mammalian G protein-coupled corticotropin-releasing factor (CRF) receptor protein or polypeptide from Rat, Mouse or human appearing as ADJ65801, ADJ65805, or ADJ65810, encoded by the nucleic acids appearing as ADJ65802, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800, ADJ65800,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New mammalian G protein-coupled corticotropin-releasing factor receptor protein, useful in diagnosing and treating Alzheimer's disease, anorexia nervosa, Cushing's disease, alcoholism, irritable bowel syndrome or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCCTCCAGGACCAGCACTGCGAGAGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Donaldson CJ,
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Location/Qualifiers
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93US-00110286.
94WO-00305908.
94US-00353537.
95US-00483139.
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P-PSDB; ADJ65797.
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09-DEC-1994;
07-JUN-1995;
12-NOV-1998;
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23-AUG-1993;
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The present invention relates to the isolation of novel CDNA sequences which encode human secreted proteins. The CDNA sequences have been derived from a variety of human tissues. The invention also provides a method for producing proteins from these polymuclectide sequences. The proteins are useful for identifying compounds that modulate their action and the cell is also useful for identifying compounds that modulate expression of the polymuclectide sequences of compounds the secreted proteins. The sequences of the invention are useful for treating diseases such as hyperproliferative disorders (e.g. cancer), immune deficiency disorders (e.g. severe combined immunodeficiency (SCID)), autoimmune disorders (e.g. multiple sclerosis), blood disorders (e.g. thrombocytopaenia), inflammatory disorders (e.g. arthritis) and the invention are also useful in gene therapy. AAS62214-AAS62838
1294 AGCTTTCACAGCATCAAACAGTCCACAGCAGTCTGAGCTGGCAGGTCATGGAGCAGCCCC 1353
                                                1500
                                                                  1414 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGAGGGG 1473
                                                                                                                   1501 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGGGGGG 1560
                                                                                                                                                                                                                                                                                                                                                                                                                                                Human secreted protein; hyperproliferative disorder; autoimmune disorder; immune deficiency disorder; blood disorder; inflammatory disorder; infectious disorder; gene therapy; antimicrobial; hepatotropic; immunosuppressive; antirheumatic; ss.
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                                                1441 CAAAGAGCTGTGGGGGGGATGACGGCCAGGCTCCCTGACCACCCTGTGGAGGT
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Gulukota K, Graham JR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotides encoding secreted proteins useful for treating asthma, HIV and Crohn's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA sequence #30 encoding novel human secreted protein.
                                                                                                                                                                                                              1474 CCGCTCTCCCCCTGCAGCCGTG 1495
                                                                                                                                                                                        1561 CCGCTCTCCCCCTGCAGCCGTG 1582
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                                                                                                                                                                                                                                                                                                               AAS62243 standard; cDNA; 2579
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                                                                                     2420 CGAGCCGCCGCCGCCGCCGCTTCCTCTGGATGTCCCGTAGGACCCGGGCATTCAGGAC
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                                                                                                                                           2360 GGTAGCCGAGCGAGGAGGATGGGAGGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTT
                                                                                                                                                                                        CTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCCTCCAGGACCAGCACTGCGAGAGGCCTG
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Best Local Similarity 94.5%;
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Human GPCR CRHR1 polynucleotide, SEQ ID NO:953. ADO29851 standard; cDNA; 2536 BP (first entry) 29-JUL-2004 AD029851; RESULT 12 AD029851 

G protein-coupled receptor; GPCR; drug screening; diagnosis; transgenic mouse; neurological disorder; adrenal gland disorder; cardiovascular disorder; intestinal disorder; cardiovascular disorder; intestinal disorder; cardiovascular disorder; blood disorder; immune disorder; bone disorder; cancer; citt disorder; metabolic disorder; nutritive disorder; cancer; widney disorder; uterus disorder; nutritive disorder; cancer; ene; ss.

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TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACC

WO20040400000-A2

13-MAY-2004

09-SEP-2003; 2003WO-US028226.

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The invention relates to human and mouse G protein-coupled receptors (GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the inventing, preventing or diagnosing diseases. Compounds useful in the treatment of GPCR-related diseases, a transgenic compounds useful in the treatment of GPCR-related diseases, a transgenic mouse comprising a GPCR transgene or in an endogenous GPCR gene; cells derived from the trasngenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising comprising a GPCR nucleic acid. The GPCR nucleic acid and proteins may be used in the diagnosis, treatment or prevention of a wide variety of comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, distrances, food poisoning or irritable bowel associated infarction; muscular disorders (e.g., angina, cardiac arrhythmia or mydrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or syndrome); bone and joint disorders (e.g., angina, cardiac arrhythmia or anemia or leukaemia); menume disorders (e.g., autoimmune disorders or ALDS); bone and joint disorders (e.g., autoimmune disorders or ALDS); bone and joint disorders (e.g., autoimmune disorders or consens); netabolic or nutritius, mayme deficiency-related diseases or vitamin deficiency-related diseases); and disorders or the kidney, liver, lung, breast, ovary, uterus, prostate, testis skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from NIPO at ceptoporaries.
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                                                                                                                                                                                                                                                                                                        Novel mammalian G protein coupled receptors, useful for identifying
                                                                                                                                                                                                                                                                                                                                compounds that modulates diagnosing and treating disease condition associated with GPCR dysfunction e.g. autoimmune diseases, angina
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                                                                                                                                                   Li F;
Zeng H;
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Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D,
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                                                                                                                                                                                                                                                                                                                                                                                   pectoris, Parkinson's disease.
                        09-SEP-2002; 2002US-0409303P. 09-APR-2003; 2003US-0461329P.
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                                                                                                (PRIM-) PRIMAL INC
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The invention relates to identifying candidate compounds for regulating skeletal muscle mass or function, comprising contacting a test compound with vertebrate corticotropin releasing factor 2 receptors (CRP 2 R), determining if the compound binds to or activates CRF2R, selecting compounds that bind or activate CRF 2 R, and determining if compound increases muscle mass or function in muscle arrophy model. Also included are identifying candidate therapeutic compounds from a group of one or more candidate compounds which have been previously determined to bind to or activate a vertebrate CRF 2 R (comprising administering the candidate compound to a non-human animal and determining whether the candidate compound regulates skeletal muscle mass or function in the treated animal), increasing skeletal muscle mass or function in a subject in which such an increase is desirable (comprising identifying subject in which an increase in muscle mass or function is desirable and administering to the subject a safe and effective amount of a CRF 2 R
                                                                                                                                                                                                                                                  1559 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGGCACTGACAGCCTGGAGGGG 1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying compounds for regulating skeletal muscle mass or function, by contacting test compound with vertebrate corticotropin releasing factor2 receptors (CRF2R), selecting compounds that bind or activate CRF2R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; 88; gene; corticotropin releasing factor receptor; CRF1R; CRF2R;
1379 CACTCGATCCGTGCCCGAGTGGCCCGTGCCATGCCCATCCCCACCCCCCAACCCGTGTC
                                                                                                    1439 AGCTTTCACAGCATCAAGCAGTCCACAGTCTGAGCTGGCAGGTCATGGAGCAGCCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human corticotropin releasing factor receptor 1, CRF1R, cDNA
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P-PSDB; ADOS0783.
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                       386 TGCCCGCCGCAGCCCTGCGGGGCCAGCTAGTGCTTCGGCCTCCTGCCTTTTTCTAT
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immunopathy; AIDS; asthma; neuropathy; Alzheimer's disease; microarray.
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agonist), a purified antibody specific for a CRPZR (where the antibody is a chimaeric or human antibody), and a pharmaceutical composition comprising a safe and effective amount of a CRPZR agonist and carrier. The methods are useful for identifying candidate compounds for regulating skeletal muscle mass or function, for increasing skeletal muscle mass or function, for increasing skeletal muscle mass or identifying candidate compounds that are potentially useful in the treatment of skeletal muscle dystrophy and for identifying compounds that prolong or augment the agonist-induced activation of CRPZR or of a CRPZR signal transduction pathway. The compound is useful for treating skeletal muscle hypertrophy and for modulating skeletal muscle hypertrophy and for modulating skeletal muscle atrophy induced by e.g. surgery, bed rest, broken bones, infectious disease or AIDS cachexia. The present sequence encodes a corticotropin releasing factor
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Pred. No. 0;
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                        361 ATCATCAACTACCTGGGCCCACTGTATCTCCCTGGTGGCCCTCCTGGTGGCCTTTGTCCTC
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                                                                                                                                                                                                              GTGGGGGCTCCATGGAGTGCCCCCATTTCAGGTTCGAAGGAGCATCCGGTGCCTGCGA
                                                                                                                                                                                                                                                                                AACATCATCCACTGGAACCTCATCTCCGCCTTCATCCTGCGCAACGCCACCTGGTTCGTG
                                                                                                                                                                                                                                                                                                        GTCCAGCTAACCATGAGCCCCGAGGTCCACAGAGCAACGTGGGCTGGTGCAGGTTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a combination which, comprises a number of polynucleotide probes comprising a sequence selected from one of the 1490 sequences mentioned in the specification. The combination is useful as an array element in a microarray for monitoring the expression of a number of target polynucleotides. The microarray is particularly useful in the diagnostics and treatment of cancer and immunopathology and neuropathology. The microarray is useful in diagnostics and treatment regimens, drug discovery and development, toxicological and carcinogenicity studies, of cremsics and pharmacogenomics. The microarray is also useful for monitoring progression of diseases and for developing sophisticated profiles for the effects of currently available therapeutic drugs. The combination is also useful for purifying a subpopulation of mRNNs, cDNAs and genomic fragments and in research and diagnostic applications. The carray can detect changes in expression in a large number of genes coding for different signaling pathway populations which can be used to diagnose various diseases including cancer e.g. adenocarcinoma and leukaemia.

Can partinson's disease. The present sequence represents a polynucleotide probe of the invention. Note: The sequence represents a polynucleotide formet directly from USPTO et. The sequence data for this patent did not format directly from USPTO et.
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                                                                                                                                                                                                                                                                                                                         Combination of polynucleotide probes, useful as array elements in microarray for monitoring the expression of a number of target polynucleotides.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1335 BP; 249 A; 432 C; 350 G; 304 T; 0 U; 0 Other;
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84.4%; Score 1335; DB 10;

Best Local Similarity 100.0%; Pred. No. 3.5e-313;

Matches 1335; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seqdata.uspto.gov/sequence.html?DocID=06500938B1
                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1360; 65pp; English.
                                                                                                                                        98US-00016434
                                                                                         98US-00016434
                                                                                                                                                                                      (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                 Seilhamer JJ;
                                                                                                                                                                                                                                                                                WPI; 2003-352189/33
                                                                                         30-JAN-1998;
                                                                                                                                        30-JAN-1998;
US6500938-B1
                                                                                                                                                                                                                                    Au-Young J,
                                              31-DEC-2002
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Human; probe; 88; receptor-like polypeptide; transducing polypeptide; defector-like polypeptide; cancer; immunopathology; neuropathology; drug development; toxicology; carcinogenicity; signalling pathway polypeptide; adrenal gland; bladder; bone; signalling pathway polypeptide; adrenal gland; bladder; bone; bone marrow; brash; breast; cervix; tumouri immunopathology; AlDS; diabetes; pancreatitis; osteoporosis; ulcerative colitis; neuropathology; dementia; amnesia; epilepsy; Alzheimer's disease; depression.
                                 Human polynucleotide probe #1360
                                                                                                                                                                                26-NOV-2002; 2002US-00305720
                                                                                                                                                                                                                  (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                    Seilhamer JJ;
                 (first entry)
                                                                                                                                                                                                                                                      WPI; 2004-090520/09.
                                                                                                                                            US2004010136-A1
                                                                                                                            Homo sapiens.
                                                                                                                                                                                                 30-JAN-1998;
                 22-APR-2004
                                                                                                                                                                                                                                    Au-Young J,
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GTGGGGGCTCCATGGAGTGGTGCCCCATTTCAGGTTCGAAGGAGCATCCGGTGCCTGCGA

AACATCATCACTGGAACCTCATCTCCGCCTTCATCCTGCGCAACGCCACCTGGTTCGTG

GTGGGGGCTCCATGGAGTGGCCCCCATTCCAGGTTCGAAGGAGCATCCGGTGCCTGCGA

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541 AACATCATCACTGGAACCTCATCTCCGCCTTCATCCTGCGCAACGCCACCTGGTTCGTG GTCCAGCTAACCATGAGCCCCCGAGGTCCACCAGAGCAACGTGGGCTGGTGCAGGTTGGTG GTCCAGCTAACCATGAGCCCCCGAGGTCCACCAGAGCAACGTGGGCCTGGTGCAGGTTGGTG

621

TTTCTGCGGCTCAGGCCAGGCTGCACCATTGGGGTGACCAGGCAGATGGAGCCCTGGAG

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GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAGCAAGGTGCCACTACCATGTCGCAGTC ATCATCAACTACCTGGGCCCACTGTATCTCCCTGGTGGCCCTCCTGGTGGCCCTTTGTCCTC

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AACAATGGCTACCGGGAGTGCCTGGCCAATGGCAGCTGGGCCGCCCCCGCGTGAATTACTCC GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAGGCAAGGTGCACTACCATGTCGCAGTC

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The invention relates to a composition of polynuclectide probes

comprising first polynucleotide probes comprising at least a portion of a

comprising at receptor-like polypeptide, second polynucleotide probes

comprising at least a portion of a gene encoding at transducing

colypeptide and third polynucleotide probes comprising at least a portion

composition are useful as array elements in a microarray for monitoring

the expression of target polynucleotides. The microarray is useful in the

composition are useful as array elements in a microarray for monitoring

the expression of target polynucleotides. The microarray is useful in the

composition and treatment of cancer, an immunopathology or a

neuropathology. It can also be used for drug discovery and development,

contrological and carcinogenicity studies, forensics or pharmacogenomics.

Contrological and carcinogenicity studies, forensics or pharmacogenomics.

Microarrays can also be used for monitoring the progression of diseases

contrological and carcinogenicity studies, forensics or pharmacogenomics.

Microarrays can also be used for monitoring the progression of diseases

confloyentides. The composition can also be used to purify a subpopulation

confloyentides. The composition can also be used to purify a subpopulation

confloyent in the disgnosis and treatment of cancer, e.g. cancers of

the adrenal gland, bladder, bone, bone marrow, brain, breast or cervix,

confloyent and munopathology, e.g. AlDS, diabetes, pancreatitis, osteoporosis or

confloyent dispanse or depression. This sequence represents a

confloyent dispanse or depression. This sequence data for

confloyent dispanse to the printed specification but was

confloyed the patent did not form part of the printed specification but was New composition comprising polynucleotide probes, useful as array elements in a microarray for monitoring the expression of target polynucleotides or purifying a subpopulation of mRNAs, cDNA, or genomic Claim 6; SEQ ID NO 1360; 73pp; English seqdata.uspto.gov/sequence.html.

Length 1335; Sequence 1335 BP; 249 A; 432 C; 350 G; 304 T; 0 U; 0 Other; Ouery Match
84.4%; Score 1335; DB 12;
Best Local Similarity 100.0%; Pred. No. 3.5e-313;
Matches 1335; Conservative 0; Mismatches 0;

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1222 GAAICCTICCAGGGCTICTITGIGICIGIGITCTACTGITICCTCAATAGIGAGGICCGT 1162 GICAAICCCGGGGGAIGAGGICICCCGGGICGICITCAICTACTICAACTICCTICGTICCTG 셤 ઠ 8

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1102 GCTGTGAAAGCCACTCTGGTGCTGCTGCCCTCTGGGCATCACCTACATGCTGTTCTTC 1021 GCTGTGAAAAGCCACTCTGGTGCTGCTGCTCTGGGCATCACCTACATGCTGTTCTTC

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Db 1141 GAATCCTTCCAGGGCTTCTTTGTGTCTTACTGTTTCCTCAATAGTGAGGTCCGT 1200

Qy 1282 TCTGCCATCCGAAAAGTGGCACGGCAGGCAGACCTCGATCCGTCGCCGAGTG 1341

Db 1201 TCTGCCATCCCGAAGAGGTGCCACGTGGCAGACACTCGATCCGTGCCCGAGTG 1260

Qy 1342 GCCCGTGCCATGTCCATCCCCCACCTCCCAACCGTGCCATCCGAGTG 1260

Db 1261 GCCCGTGCCATGTCCATCCCCCACCTCCCCAACCGTTTCACAGCATCAAGCAG 1401

Db 1261 GCCCGTGCCATGTCCATCCCCACCTCCCCAACCGTGTCAGCTTTCACAGCATCAAGCAG 1320

Qy 1402 TCCCACAGCAGTCTGA 1416

Db 1321 TCCACAGCAGTCTGA 1335
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Search completed: March 17, 2006, 10:52:33 Job time : 1006 secs

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Title: Perfect score:

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100.0%; Score 1582; DB 6; Length 1582;
Best Local Similarity 100.0%; Pred. No. 2.5e-287;
Matches 1582; Conservative 0; Mismatches 0; Indels 0;
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1 (bases 1 to 1582)
Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Sawchenko,P.
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LOCUS DEFINITION Sequence 14 from patent US 6638905. ACCESSION AR412107 VERSION AR412107.1 GI:4016466 KEYWORDS SOURCE ORGANISM Unknown. ORGANISM Unknown. Unclassified. REFERENCE TITLE Cloning and recombinant production of CFR receptor(8) AUTHORS SAWCHENCYP. TITLE Cloning and recombinant production of CFR receptor(8) AUTHORS LOCATION AG88905-A 14 28-OCT-2003; THE Salk Institute for Biological Studies; La Jolla, CA Location/Qualifiers 1 .1582	Owner Match  Query Match  Query Match  Best Local Similarity 100.0%; Pred. No. 2.5e-287;  Matches 1582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Qy 1 CGAGCCGCCGGCCGGTTCCTCTGGGATGTCCGTAGGACCGGGCATTCAGGAC 60	GTAGCCGAGCCCGAGGAGGGGCCCCCCCCGCAGCTCCGTCTCGTCAAGGCCCTT 120	Qy         181 TCCCTGGCCAGCAACATCTCAGAACTGCAACGCATCCGTGGACCTCATTGGCACC 240           Db         181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACC 240           Qy         241 TGCTGGCCCGCAGCCCTGCGGGGCAGCTAGTGGTTCGGCCTGCCT		Db 421 GTGCACTACCATGTCATCATCATCATGGGGCACTGTATCTCCCTGGTGGCC 480  Qy 481 CTCCTGGTGGCCTTTGTCCTTTTCTGCGGCTCAGGCTGCACTGTATCTCCCTGGTGGCC 540  481 CTCCTGGTGGCCTTTGTCCTTTTCTGCGGCTCAGGCTGCACCCATTGGGGTGAC 540  481 CTCCTGGTGGCTGCTGCTGCTGGGGGGCTCAGGCTGCACCCATTGGGGTGAC 540  Qy 541 CAGGCAGATGGAGCCTGGAGGTGGGGGCTCCATGGAGCTGCACCCATTCAGGTTCGA 600  Db 541 CAGGCAGATGGAGCCTGGAGGTGGGGGCTCCATGGAGCTGCCCATTTCAGGTTCGA 600  Qy 601 AGGAGCTCCTGGAAGGTGGGGGGTCCATGGAACCTCCTCTCTCCGCTTTCAGGTTCGA 600  Qy 601 AGGAGCACTGGTGCTGCGAAACATCATCACCATGGAACCTCCTCTCTCCGCTTTCTTCTG 600  Qy 661 CGCAACGCCACTGGTACCTGCAAACATCATCACCATGAACCTCACCAGAGCAAC 720  Ell
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Best Local Similarity 94.5%; Pred. No. 1e-252;
Matches 1495; Conservative 0; Mismatches 0;
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Patent: US 6399315-A 1 04-JUN-2002,
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/mol_type="unassigned DNA"
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1 (bases 1 to 1495)
Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and
Sawchenko,P.
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AR211440 1495 bp Sequence 1 from patent US 6399315. AR211440

GI:21514762

AR211440.1 Unknown. Unknown

RESULT 5
AR211440
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE AUTHORS

840

753

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1 CGAGCCGCAGCCGCCCGCCGGTTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC 60	1	61 GGTAGCCGAGCGCCGAGGATGGGAGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTT 120	61 GGTAGCCGAGCCCGAGGATGGGAGGGCACCCGCAGCTCCGTCTGTCT		181 TCCCTGGCCAGCAACATCTCAGGACTGCAACGCATCCGTGGACCTCATTGGCACC 240	241 TGCTGGCCCCGCAGCCCTGCGGGGCAGCTAGGGGTTCGGCCCTGCCCTTTTTTCTAT 300	241 Iderogetetetagetetagegagetagegagetregetetetetetretetr		361 GCGCCCGGGTGANTTACTCCGAGTGCCAGGAGATCCTCANTGAGGAGAAAAAAAG 420 	GTGCACTACCATGTCGCAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 4	GTGCACTACCATGTCGCAGTCATCATCATACCTGGGCCACTGTATCTCCCTGGTGGCC 48	481 CICCAGAIGACCITITGACCACTATACTAGGACTAGGCAGGCTGCACCCATTGGGGTGAC 540 481 CICCAGGCACCCATTGGGGTGAC 540	CAGGCAGATGGAGCCCTGGAGGTGGGGGCTCCATGGAGTGGTGCCCCCATTTCAGGTTCGA	514 513	AGGAGCATCCGGTGCCTGCGAACATCATCCACTGGAACCTCATCTCCGCCTTCATCCTG	AGGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCCGCCTTCATCCTG 57	661 CGCAACGCCACCAGGTTCGTCACCTAACCCCCCGAGGTCCACAGAGGTCCCAGAGGTCCCAGAGGTCCCAGAGGTCCAGAGGTCCAGAGGGTCCAGAGGTCCAGAGGTCCACGAGGTCCACGAGGTCCACCAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACCAGAGGTCCACCAGAGGTCCACCAGAGGTCCACAGAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGGTCCACAGAGAGAG	721 Gradacradaradaradacadacagacaracracracracrataraacaacaratra 780 	781 IGGAIGITCGGCGAGGGCTGCTGCACCACCACCGTGCTCACCTACTCCACTGAC 840	redangircededadederideracerdedacacadecarestraceracitedacerda	841 CGGCTGCGCAAATGGATGTTCATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTG 900	GCCTGGGCCATTGGGAAGCTGTACTACACAATGAGAAGTGCTGGTTTGGCAAAAGGCCT		951 GGGGTGTACACCAGTTACACCAGGCCCCCATGATCCTGCTGCTGCTGATCATTC 1020 874 GGGGTGTACACCGACTACATCTACCAGGCCCCCATGATCCTGGTCCTGCTGATCAATTTC 933	1021 ATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGGATCCACCACGTCT 1080	934 ATCHTCCTTTTCACATCGTCCGCATCCTCATGACCAAGCTCCGGGGCATCCACCACGTCT 993
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121 CTCCTTCTGGGGCTGAACCCCGTCTCGCCTCCCCGGGACCAGCACTGCGAGGCCTG 180  181 TCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCGTGGACCTCATTGGCACC 240  181 TCCTGGCCAGCAACATCTCAGGACTGCAGTGCATCGTCGTGGACCTCATTGGCACC 240  241 TGCTGGCCCGCAGCCCTGCGGGACTGCAGTGGTTCGGCCCTGCCCTTTTTTCTAT 300  241 TGCTGGCCCCGCAGCCCTGCGGGACTAGTGGTTCGGCCCTGCCCTGCCTTTTTTCTAT 300  301 GGTGTCCGCTACAATACCACAACAACAACGGAGTTCGGCCCTGCCCTGCCTTTTTTCTAT 300  301 GGTGTCCGCTACAATACCACAACAACAACGGAGATCGGCCTGCCT	CGCAACGCCACCTGGTTCGTGGTCCAGCTAACCATGAGCCCCGAGGTCCACCAGGGAACCACCAGGCAACCGCAACGCCACCAGGGTCCACCAGGGAACCATGAGCCCCGAAGGTCCACCAGGGTCCAGGTTAACCATGAGCCCCGAAGGTCCACCAGGGCAACTTCTTCCATGTGACCAGGTTGGTGACAGCCGCCTACAACTACTTCCATGTGACCAACTTCTTCTTCGTGACCAGGTTGGTGACAACTACTTCCATGTGACCAACTTCTTCTTCGTGACCAGGTTGGTGACAGCCCTACAACTACTTCCATGTGACCAGGTTGGTGACAGCCTACACATCTTCTTCTTCGGGGGGGG	GCCTGGGCCATTGGGATGTTCATCTGCATTGGCTGGGTGTGCCCTTCCCCATCATTGTG GCCTGGGCCATTGGGAAGGTGTACTACGCATGGCTGGGGGTGTGCCCTTCCCCATCATTGTG GCCTGGGCCATTGGGAAGCTGTACTACGATGGAAGGAGTGTCCTGGTTTGGCAAAAGGCCT GCGTGTACACCGACTACACAATGAAAGAAGTGCTGGTTTGGCAAAAAGGCCT GCGTGTACACCGACTACACACAATGAAAAGAAGTCCTGGTTTGGCAAAAAGGCCT GCGTGTACACCGACTACACACAATGAAAAGCCCCATGATCTGGTTTTGCAAAAAAGCCT ATCTTCCTTTTCAAAATCGTCGCATCCTCATGACCAAGGCTCTGGTGTTTTTCAAATTTCAACATCGTCGCATCCTAGACCACACGTCT ATCTTCCTTTTCAAAAACCCATCCTCAAAACACAAACACAAGGCTCTGGTGTTTTCAATTTCAACATCAGAAGCTCTCAAAAACAAAACAAAACAAAACAAAACAAAACAAAAAA
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301 GGTGTCCGCTACAATACCACAAAGGCTACCGGGAGTGCCTGGCCAATGGCTGG 360	361 GCCGCCCGCGTGAATTACTCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAA	421 GTGCACTACCATGTCGCAGTCATCAACTACCTGGGCCACTGTATCTCCCTGGTGGCC 480	481 CTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGGCTGCAGCTGCACTTGGGGTGAC 540	541 CAGGCAGATGGAGCCCTGGAGGTGGGGCTCCATGGAGTGCTGCCCCATTTCAGGTTCGA 600	AGGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCCGCCTTCATCCTG	514 AGGAGCATCCGGTGCCTGCGAAACATCATCCACTGGAACCTCATCTCCGGCCTTCATCCTG 5/3 661 CGCAACGCCACCTGGTTCGTGGTACCTAACCATGAGCCCCGAGGTCCACCAGAGCAAC 720 671 CACAA CGCCAACGATCCAGCTAACCATGAGCCCCGAGGTCCACCAGAACAAC 720 671 CACAA CGCCAACAACAACAACAACAACAACAACAAACA	GTGGGCTGCTGCTGGTGCTGCTGCTGCTACATTGACCCCCGAGGTCCCCCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCCCAGGTCGCTGCTGCTGCTGCTGCCGCCTGCAACTACCTTCCATGTGACCAACTTCTTC	781 TGGATGTTCGGCGAGGCTGCTACCTGCACACACGCCATCGTGCTCACCTACCT	841 CGGCTGCGGAAATGGATGTTCATCTGCATTGGCTGGGGGTGTGCCCTTCCCCATCATTGTG 900	901 GCCTGGGCCATTGGGAAGCTGTACTACGACAATGAGAAGTGCTGGTTTGGCAAAAGGCCT 960 	961 GGGGTGTACACCGACTACATCTACCAGGGCCCCATGATCCTGGTCCTGCTGATTCATTC	1021 ATCTTCCTTTTCAACATCGTCCGCATCCTCATGACCAAGCTCCGGGCATCCACGTCT 1080	1081 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCTGCTCCTCGGGC 1140		1201 ATCTACTTCATCCTTCCTGGAATCCTTCCAGGGCTTCTTTGTGTCTGTGTTCTACTGT 1260	1261 TTCCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320 	1321 CACTCGATCCGTGCCCGAGTGGCCCTGCCATGTCCATCCCCACCTCCCCAACCCGTGTC 1380	1381 AGCTTTCACAGCATCAAGCAGTCCACAGCAGTCTGAGCAGCTCATGGAGCAGCCCC 1440
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Qy 1261 TICCTCAATAGTGAGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCAGGACAAG 1320	bb 1174 TTCCTCAATAGTGAGGTCCGTTCTGCCATCCGAAGAGGTGGCACGGTGGCAGGACAAG 1233  Oy 1321 CACTCGATCCGTGCCCGAGTGGCCCGTGCCATGTCCATCCCACCTCCCCACGTGTC 1380	Db 1234 CACTCGATCGTGGCCGAGTGGCCGTTCCCTCCCCCCCCCC	Db 1294 AGCTTTCACAGCTCAAGCAGCTCAAGAGCTGAGCTGACTCATGAGCACCCC 1353  Qy 1441 CAAAGAGCTGAGGGAATAACGCCCAGGCTCCCTGACCTCACGCCGAGGGT 1500	Db 1354 CAAAGAGCTGTGGCTGGGGGATGACGGCCAGGCTCCCTGACCTCCTGTGTGGAGGT 1413	1414 GACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCAGCATGACAGCCTGGGGGGGG	Db 1474 CCGCTCCCCTGCAGCGTG 1495	RESULT 8 AR412100 LOCUS AR412100 LOCUS AR412100 DEFINITION Sequence 1 from patent US 6638905.		OKGANISM UNCLABBILITED.  REFERENCE 1 (bases 1 to 1495) AUTHORS Perrin,M.H., Chen,R., Lewis,K.A., Vale,W.W. Jr., Donaldson,C.J. and	н	FEATURES LOCALLOH/QUALILLEIB  SOUICE 1. :1495 /organism="unknown" /mol_type="genomic DNA"	Query Match  Query Match  Best Local Similarity 94.5%; Pred. No. 16-252;  Matches 1495; Conservative 0; Mismatches 0; Indels 87; Gaps 1;		Oy         61         detracedadecedadecedadargadadadadadadacacacececacacereregreaadacerr         1	Oy 121 CTCCTTCTGGGGCTGAACCCGTCTCTGCCTCCAGGACCAGCACTGCGAGAGCCTG 180  121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCAGGACCTGCGAGAGCCTG 180	181 TCCTGGCCAGCAACATCTCAGGACTGCAGGCCATCCGTGGACCTCATTGGCACC	241 TGCTGGCCCCGCAGCCTGCGGGCAGCTAGTGGTCGCCCTGCCCTGCCTTTTTCTAT	Db 241 TGCTGGCCCCGCAGCCTGCGGGGCCAGCTAGTGGTTCGGCCCTGCCTTTTTCTAT 300 QY 301 GGTGTCCGCTACAATACCACAAACAATGCCTACCGGGAGTGCCTGGCCAATGGCAGCTGG 360

481 CTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGGCCAGGCTGCACCCATTGGGGTGAC 54  [1	00   00   00   00   00   00   00   0	021 ATCTTCCTTTTCAACATCCTCCCCATCATCACCAGCCTCCCGGCCATCCACCACCTCT   1138     1079 ATCTTCCTTTTCAACATCGTCCGCATCCTCTGGTCCTCCGGCCATCCACCACCTCT   1138     1081 GAGACCATTCAGTACAGGAAGGCTCTTCATGGTCGTCTCCCCGCCACCTCTTGGTC   1138     1139 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTCGTCGCTCCTCTGGCC   1138     1141 ATCACCTACATCCTCTTCATCCTCGAACACTCTGGTGCTGCTCCCTCTGGCC   1138     1159 ATCACCTACATCCTTCTTCGTCAATCCCTGGGGAAGATCAGGTCTCTCTGTTCTTTCT
1294 AGCTTTCACAGCATCAAGCAGTCCACAGCAGCTGGCAGGTCATGAAGCAGCCCC   1353     1441   CAAAGAGCTGTGGCTGGGGGATGACGGCTCGCCTGACCCTGCTGGAGGT   1500     1354   CAAAGAGCTGTGGGTGGGTGAAGGTCCCTGACCCTGCCTG	RESULT 9  AR442670 LOCUS AR442670 AR442670 ACCESSION AR442670 ACCESSION AR442670 ACCESSION AR42670 AR442670 AR4	Query Match   88.3%; Score 1336.4; DB 6; Length 2536; Best Local Similarity   94.4%; Pered. No. 1.96-252; Indels 87; Gaps 1; Matches 1494; Conservative 0; Mismatches 1; Indels 87; Gaps 1; Accessorative 0; Mismatches 1; Indels 87; Gaps 1; CadaCccacacacacacacacacacacacacacacacaca

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   446 GGTGCCGCTACAATACCACAAACAATGCCTACCGGGAGTGCCTGGCCAATGGCAGCTGG
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                                                                                                                                                                                               HSCRFA 17-FEB-1997 H. Bapiens mRNA linear PRI 17-FEB-1997 H. Bapiens mRNA for corticotrophin releasing factor receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vita, N., Laurent, P., Lefort, S., Chalon, P., Lelias, J.M., Kaghad, M., Le Fur, G., Caput, D. and Ferrara, P. Termary structure and functional expression of mouse pituitary and human brain corticotrophin releasing factor receptors
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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Opdenakker,G., Fiten,P., Nys,G., Froyen,G., Van Roy,N.,
Speleman,F., Laureys,G. and Van Damme,J.
The human MCP-3 gene (SCYA7): cloning, sequence analysis, and
assignment to the C-C chemokine gene cluster on chromosome
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                                                                                                                                                                                                                                                                                                                        corticotropin releasing factor receptor. Homo sapiens (human) Homo sapiens
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/organism="Homo sapiens"
/mol type="mkNx"
/db_xref="taxon:9606"
/tissue_type="brain"
227. 1474
/codon_start=1
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NASVDLIGTOWPRSPAGGLVVRPCPRFFYGYRYNTTNMGYBECLANGSWAARVNSGC
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CFLNSEVRSAIRKRWHRWQDKHSIRARVARAMSIPTSPFTVSFFYSFTVSF
                                                                                                           1335 bp mRNA linear PRI 22-OCT-1993 Human corticotropin releasing factor receptor mRNA, complete cds. L23333
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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1 (bases 1 to 1335)
Chen, R., Lewis, K.A., Perrin, M.H. and Vale, W.W.
Expression cloning of a human corticotropin-releasing-factor
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84.4%; Score 1335; DB 8; Length 1335;
Best Local Similarity 100.0%; Pred. No. 7.5e-241;
Matches 1335; Conservative 0; Mismatches 0; Indels 0
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/mol_type="mRNA"
/db_xref="taxon:9606"
/fissue_type="Human Corticotrope Adenoma"
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protein id="AAA35719.1"
db_xref="GI:408692"
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Homo sapiens (human)
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Ζ Σ	AUTHORS OBBIDGA,Y., IKeda,Y., Chaki,S. and Okuyama,S.  TITLE Monkey corticotropin releasing factori receptor: cDNA cloning and JOURNAL Unpublished  REFERENCE 2 (bases I to 2374)  TITLE Direct Submission JOURNAL Submitted (16-JAN-2002) Yuichi Oshida, Medicinal Research Laboratorise, Taisho Pharmaceutical Co.,Lid., Medicinal Pharmacology Laboratory: 1-403, Voshino-cho, Saitama	330-8530, Japan (R-mail:y.oshida@po.rd.taisho.co.jp,	gene 1. 72374  CDS 31. 1278  Acodon_start=1  /product="corticotropin releasing factor receptor type 1" /db xref="G1:88026781:1"	/translation="warhpolrlukluklilginpusasioodicesiselasnisgiloc Nasydligtcwprspragoluvprppheprygurytmorpreclangswarnysec Obilaneekkskvhythyaviinvrlehcislvalluklerreclangswarnysec Afilrnappervolimspevhosnvgwcrintrafwtirefwfrekrecktitaiu Liytidinrepelmyrythyamigelgowytpinytogpm Ilvlinrepelmyrythyastysetioorkavkatullehcitymepungedbusrvyptypyrogpm Ramsiptspruypixgstrum	Query Match         81.2%;         Score 1283.8;         DB 8;         Length 2374;           Query Matches Id11;         Conservative 0;         Mismatches 32;         Indels 88;         Gaps 2;           S2 ATTCAGGAGGGAGGGAGGCGAGGGAGGGAGGGAGCCGAGCTCGGTCTGTC         11         IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	112   AAGGCCCTTCTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCCTC	232 ATTGGCACCTGCCGCAGCCCTGCGGGGCAGCTAGTGGTTCGGCCCTGCC 291

Oy 601 AGGAGCATCCGGAGAACATCATCCACTGGAACCTCATCTCGGCTTCATCTG 660	Qy         661         CGCAACGCCACCTGGTTCGTGGTCCAGCTAACCATGAGCCCCGAGGTCCACCACAGGCAC         720           L	Qy         721         GTGGGCTGGTGCAGGTTCGTGACAGCCGCCTACAACTTCCATGTGACCAACTTCTTC         780           LINELLINITION         1   1   1   1   1   1   1   1   1   1	0   0   0   0   0   0   0   0   0   0	1021 ATCTTCTTTTCAACATCGTCGGCATCCTCATGACCAAGCTCCGGGCATCCACCACGTCT	DD 1914 AGACCATTCAGGAAGGCTGTGAAGCCACTCTGGTGCTGCCCCCTCCTGGGGGC 1140  DD 994 GAGACCATTCAGTACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCCCCTCCTGGGC 1053	1054 ATCACCTACATCCTTCCTACAATCCTTCCAGGGCATCTTTTTTTT	1114 ATCTACTTCAACTCCTTGCAAATCCTTCCAGGGCTTCTTGTGTGTTCTACTGT	1261 TICCICATIAGICAGICCGITCICCATCAGAAAAAGAGGGGCACCGGTGGCACAAAGATTATTATTATTATTATTATTATTATTATTCCATCGCATCCGGAAGAAGGTGGGCACCGGTGGCAGAACAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGGTCCGGCAAGAAGAAGGTCCGGCAAGAAGAAGGTCCGGCAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAAGAA	1321 CACTCGATCCGTGCCCGAGTGGCCCGTGTCCATCCCCACCTCCCCAACCCGTGTC 1	1381 AGTTTTCAGGATCAAGGAGTCCACA 1294 AGCTTTCACAGCATCAAGGAGTCCACAC	Db 1354 CAAAGACTGTGGGGGGATGACG 1380	_	AR442671 AR442671.1 GI:42669940 Unknown.	ORGANISM Unknown. Unclassified. REFERENCE 1 (bases 1 to 1285) AUTHORS Isfort, R.J. and Sheldon, R.J.
Qy         1492         TGTGGAGGTGACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGACAGC         1551           Db         1354         TGTGGACGCGACCTGTTAGGTCTCATGCCCACTCCCCCAGGAGCAGCTGACAGCTGACAGC         1413	Qy         1552         CTGGGGGCCGCTCTCCCCTGGAGCCGTG         1582           Db         1414         CT-GGGGGCCACTCTCCCCCTGCAGCTGTG         1443	RESULT 14 192584 LOCUS LOCUS DEFINITION Sequence 1 from patent US 5728545. ACCESSION 192584.1 GI:3937054	ADJUNCAN  ONGANISM Unknown.  ORGANISM Unknown.  Unclassified.  ND CASSERING TO CASSES TO 1380)  AUTHORS Perrin, M. H., Chen, R., Lewis, K.A., Vale, W. W. Jr. and Donaldson, C.J.  TITLE Clouing and recombinant production of CRF receptor (8)  JOURNAL Patent: US 5728545-A 1 17-MAR-1998;  FEATURES 1. 1380  ADJUNCAN ADJUNCOWN.  ADJUNCOWN.  MOLLYPOE"UNASSIGNED DNA"	ORIGIN  Query Match Query Match Best Local Similarity 94.1%; Pred. No. 4.5e-231; Matches 1380; Conservative 0; Mismatches 0; Indels 87; Gaps 1;	Qy         1         CGAGCCCGCAGCCGCCGGCCGGTTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC         60           bb         1         CGAGCCCGCCGGCCGGTTCCTCTGGGATGTCCGTAGGACCCGGGCATTCAGGAC         60	Qy         61         GGTAGCCGAGCGAGCCCGAGGAGCACCCGCAGGTCCGTCTCGTCAAGGCCTT         120           Db         61         GGTAGCCGAGCGAGCCCGAGGAGCACCCGCAGCTCCGTCTCGTCAAGGCCTT         120	OY 121 CTCCTTCTGGGGCTGAACCCCGTCTCTGCCTCCCTCCAGGACCTGCGAGAGCCTG 180	Oy         181 TCCCTGGCCAGCAACATCTGCAGACTGCAACGCATCCGTGGACCTCATTGGCACC         240           Db         181 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCGTGGACCTCATTGGCACC         240	Qy         241         TGCTGGCCCCGCAGCCCTGCGAGCCAGCTAGTGGTTCGGCCCTGCCCTTTTTCTAT         300           b         241         TGCTGGCCCCGCAGCCTGCGGGCAGCTAGTGGTTCGGCCTGCCT	Qy 301 GGTGTCCGCTACAATACCACAAACAATGGCTACCGGGGGGGG	Oy 361 GCGCCCGCGTGAATTACTCCGAGTGCCAGGAGTCCTCAATGAGGAAAAAAGCAAG 420	3166CC 3166CC	Oy 481 CTCCTGGTGGCCTTTGTGCGGGCTCAGGCTGCACCCATTGGGGTGAC 540	Qy 541 CAGGCAGATGGAGCCCTGGAGGCTCCATGGAGTGGTGCCCCATTTCAGGTTCGA 600  Db 514 513

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Methods for identifying compounds for regulating muscle n function using corticotropin releasing factor receptors Patent: US 6670140-A 3 30-DEC-2003;
The Procter & Gamble Company; Cincinnati, OH Location/Qualifiers
1. 1283
//organism="unknown"
/mol_type="genomic DNA"
                                                                                                                                   Query Match 75.1%; Score 1188; DB 6; Length 1285; Best Local Similarity 93.7%; Pred. No. 3.4e-213; Matches 1285; Conservative 0; Mismatches 0; Indels 87
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Search completed: March 17, 2006, 13:52:10 Job time : 8134 secs

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Search time 5882 Seconds (without alignments) 12583.673 Million cell updates/sec March 17, 2006, 10:34:58;

US-10-649-193-14 1582 Title: Perfect score: Sequence:

1 cgagcccgcagccgcccgcc......gctctccccctgcagccgtg 1582

41078325 segs, 23393541228 residues IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

82156650 Total number of hits satisfying chosen parameters:

Searched:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

gb\_est1:: gb\_htc::: gb\_htc::: gb\_est4::: gb\_est5::: gb\_est7::: gb\_gss1::: gb\_gss1::: EST:\* 9: 10: 11: Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Description	BC037967 Homo sapi	AY414327 Homo sapi	AY414328 Pan trogl	AY414329 Mus muscu	CF147820 AGENCOURT	DN396007 LIB3935-0	DR002290 TC110860	BM925912 AGENCOURT	AY406515 Homo sapi	CX955987 JGI CAAO8	AY406516 Pan trogl	CV039433 4136796 B	AY406517 Mus muscu	BU454812 603770849	CX885516 JGI CAAL2	CO958535 AGENCOURT	CO958736 AGENCOURT	BX113548 BX113548	AW967020 EST379094	BU134942 603121738	BB639598 BB639598	BU281668 603864305
B ID	4 BC037967	10 AY414327	10 AY414328	10 AY414329	6 CF147820	8 DN396007	8 DR002290	3 BM925912	10 AY406515	8 CX955987	10 AY406516	7 CV039433	10 AY406517	5 BU454812	8 CX885516	7 C0958535	7 C0958736	5 BX113548	1 AW967020	5 BU134942	2 BB639598	5 BU281668
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% Query Match	77.5	61.5	60.9	52.0	40.7	32.6	32.5	31.0	29.7	29.7	29.5	29.0	28.2	27.8	27.7	27.4	27.2	25.9	21.6	21.5	21.4	19.9
Score	1226.4	973	963.6	822.6	643.8	515.2	514.4	491.2	469.4	469.2	461.6	458.2	446	440.2	438.2	434	431	410	341.8	339.8	338	315
Result No.		7	٣	4	S	9	7	80	σ	10	11	12	13	1.4	15	c 16	17	18	19	20	21	22

clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 79 Row: p Column: 24 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 19923244 This clone has the following problem: retained intron.

R61773 yh09f12.rl	AU296413 AU296413	CX823905 JGI_CAAK3	H07088 y181g12.rl	CB795398 AMGNNUC:N	BM709844 UI-E-CQ1-	R35425 yg65f11.rl	F06999 HSC1SA041 n	BI849955 477933 MA	AA328065 EST31492	BY278495 BY278495	BY277788 BY277788	BF193539 245165 MA		CF147819 AGENCOURT	AK085854 Mus muscu	BU226164 603948633	BF547183 UI-R-C1-1	BG711051 pglln.pk0		CN054945 Salamande	BE255009 601115291	BU417469 603551163
B R61773	1 AU296413	8 CX823905	B H07088	6 CB795398	3 BM709844	8 R35425	B F06999	3 BI849955	1 AA328065	5 BY278495	5 BY277788	2 BF193539	5 BU249901	6 CF147819	4 AK085854	5 BU226164	2 BF547183	2 BG711051	7 CO958529	7 CN054945	2 BE255009 ·	5 BU417469
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314.4	312	310.6	309.8	294.6	289.6	283.2	277	254.4	234.2	231	219.4	207.8	195.6	193	192.4	191	182	174.2	158.4	153.2	152.8	152.2
23	24	25	56	27		59	30		32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

HTC 04-MAR-2003	Euteleostomi; arrhini;	th, Mammalian onal Cancer D 20892-2590,	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Tissue Producement: Life Technologies, Inc. Email: cgapbs-r@mail.nih.gov Tissue Producement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaichnersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc mgc@ndpri.nih.gov Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakenley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Blakenley,N.W., Mouffard,G.G., Breen,K., Brinkley,C., Haghighi,P., Hansen,N., Ho,SL., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Maskeri,B., Maskeri,B., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Young,A., Zhang,LH. and Green,E.D., Wiggins,L.,
linear	Vertebrata; imates; Cat	tes of Heal ffice, Nati Bethesda, M	nc. les, Inc. Consortium f Health In Brinkley, C Brinkley, C a, J., Haghi c, Laric, P. Strian, S.D. Thomas, P.J.
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2496 bp IMAGE:5764209, 691	Chordata; Cram Buarchontoglii	02) National ), Cancer Gend Drive, Room	http://mgc.nc Life Technolog Life Technolog tion: Life Tec Lip: The I.M.? Lip: The I.M.? Rarlins, E., I. Co, C., Maskeri, I. L., Walker, M.; L., Walker, M.;
BC037967 2496 bp Homo sapiens, clone IMAGE:5764209, BC037967.1 GI:23958691	Homo sapiens (human) Homo sapiens Homo sapiens Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bummalia; Butheria; Buarchontoglires; Primates; Catarrhini; Hominidae; Homo. Strausberg,R.	Direct Submission Submitted (20-SEP-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-r@mail.nih.gov Tissue Progres-r@mail.nih.gov Tissue Progres-r@mail.nih.gov Tissue Progres-ration: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site: http://www.nisc.nih.gov/ Contact: nisc.mgc@nhggi.nih.gov Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Dietrich,N.L., Masiello,C., Maskerin,B., Mastrian,S.D., McCloskey,J., Maduro,Q.L., Masiello,C., Maskerin,B., Mastrian,S.D., McCloskey,J. Maduro,Q.L., Masiello,C., Masker,M.A., Wetherby,K.D., Wiggins,L., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
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I (Dages I to 124, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G. (Janowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Todd, M.A., S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, White, T.J., Shinsky, J.J., Inferring nonneutral evolution from human-chimp-mouse orthologous
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                    pooled whole brains"
                                                                                                                                                                                                                                                                                                                                              4; Length 2496;
                                                                                                                                                                                                                                                                                                                                        Query Match
77.5%; Score 1226.4; DB 4.
Best Local Similarity 89.1%; Pred. No. 6.7e-293;
Matches 1409; Conservative 0; Mismatches 1;
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                       1. .2496,
| organism="Homo sapiens" |
| organism="Homo sapiens" |
| mol_type="mRNA" |
| db xref="texcn: 9606" |
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Pan troglodytes CRHR1 gene, VIRTUAL TRANSCRIPT, partial sequence, AX414128
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Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
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Adams, M.D. and Cargill, M. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and Cargill, T. Adams, M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. and M.D. an
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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                          922 TACTACGACAATGAGAAGTGCTGGTTTGGCAAAAGGCCTGGGGTGTACACCGACTAACATC
                                                                                                                                                                                                                                  814 TACCAGGCCCCATGATCCTGGTCCTGCTGATCAATTTCATCTTCCTTTTCAACATCGTC
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                                                                                                   ATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCTGGGCCATTGGGAAGCTG
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                       Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
Direct Submission

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA

This sequence was made by sequencing genomic exons and ordering them based on alignment.
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ilarity 80.1%; Pred. No. 4.4e-230;
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/gene="CRHR1"
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Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA.
This sequence was made by sequencing genomic exons and ordering them based on alignment.
                                                                                                                                                                                                                                                        82 ATGGGAGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTTCTCCTTCTGGGGCTGAACCCC
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                                                                   1..1248
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/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1...>1248
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/locus_tag="HGM5187"
                                                      Location/Qualifiers
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1 (Dases 1 to 1248)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, B., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Location/Qualifiers
922 TACTACGACAATGAGAAGTGCTGGTTTTGGCAAAAGGCCTGGGGTGTACACCGACTACATC
                                          754 TACTACGACAATGAGAAGTGCTGGTTTGGCAAAAAGGCCTGGGGGTGTACACCCGACTACATC
                                                                                                                                                                            814 TACCAGGCCCCATGATCCTGGTCCTGCTGATCAATTTCATCTTCCTTTTCAACATCGTC
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Mus musculus CRHR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Direct Submission
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Mus musculus (house mouse)
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Extractors, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini; Homindae; Homo.

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AL Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancitute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue procurement: GPCR Consortium

CDNA Library Preparation: GPCR Consortium

CDNA Library Arrayed by: The I.M.A.G.E. Consortium

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLML at:

http://image.llnl.gov

Plate: IRBIOZ row: D column: 09

High quality sequence stop: 738.

High quality sequence stop: 738.

Location/Qualifiers

Location/Qualifiers
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                                                                                                                                                                                                                                              /lab_hoft="DH10B"
/clone_lib="NIH_MGC_145"
/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
814 TACCAGGGCCCCATGATCCTGGTCCTGCTGATCAACTTTATCTTTCTCTTCAACATTGTC 873
                                                                                                       1102 GCTGTGAAAGCCACTCTGGTGCTGCCCCTCCTGGGCATCACCTACATGCTGTTCTTC
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/mol_type="mxNA"
/db xref="taxon:9606"
/clone="IMAGE:6971902"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAAGGAGGTGCACTACCATGTCGCAGTC
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                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                       DB 10; Length 1248;
                                                                                                                                                                                                                                                                                 87;
                                                                                                                                                                                                                 ch 52.0%; Score 822.6; DB 10; Length I Similarity 73.1%; Pred. No. 9e-193; 976; Conservative 0; Mismatches 272; Indels
   /mol_type="genomic DNA"
/db_xref="taxon:10090"
                                                             <1. ...>1248
/gene="CRHR1"
/locus_tag="HCM5187"
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Matches 976; Conserv
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32.6%; Score 515.2; DB 8; 94.1%; Pred. No. 1.4e-116; attive 0; Mismatches 33;
                                                                                                                                                                                                                                                                                            /organism="Canis familiaris"
/mol_type="mRNA"
/strain="beagle"
                                                                                                                                                                                      Direct Submission (Staten, N.R.)
Unpublished (2005)
Contact: Nick Staten
Tel: 636 247 6855
Email: nicholas.r.staten@pfizer.com.
                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9615"
/clone="CLN8913387"
                                          DN396007
DN396007.1 GI:60577228
                                                                       EST.
Canis familiaris (dog)
Canis familiaris
                                                                                                                                                           1 (bases 1 to 581)
Staten, N.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     546; Conservative
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Best Local Si
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                                         ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
               DEFINITION
                                                                                                                                                                                      TITLE
JOURNAL
COMMENT
                                                                                                                                                            REFERENCE
AUTHORS
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            pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5' ECGNV-Xml/Khoi-3', 5'-ECGNV-Xml/Khoi-3', For information about which gene each clones represents, passes visit our anonymous ftp site at ftp://image.lnl.gov/image/rearrayed_plates/IRBI.preSV.dat a Note: this is a NIH WGC Library."
                                                                                                                                                                                                        141
                                                                                                                                                                                                                                                                 201
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                                                                                                                                                                                                                                                                                                                                          155 GGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACCTGGCCCCGCAGCCCTGCG 214
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varies by clone; ORFs were PCR-amplified and cloned into
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                                                                                                                                                                                                       ATGGGAGGGCACCCGCAGCTCCGTCTCGTCAAGGCCCTTCTCCTTCTGGGGCTGAACCCC
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728 ATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGGGCTGNGCCATGG 779
                                                                                                                                                                          87;
                                                                                                                                               Length 779;
                                                                                                                                                                           Indels
                                                                                                                                             Score 643.8; DB 6;
Pred. No. 1.9e-148;
0; Mismatches 3;
                                                                                                                                             Match 40.7%;
Local Similarity 89.2%;
es 742; Conservative
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581 bp mRNA linear EST 07-MAR-2005 LIB335-011-Q6-K6-G12 LIB3935 Canis familiaris cDNA clone CLN8913387, mRNA sequence. 1153 1213 1033 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Laurasiatheria, Carnivora, Fissipedia, Canidae, 1093 CCTTCCTGGAATCCTTCCAGGGCTTCTTGTGTCTGTGTTCTACTGTTTCCTCAATAGTG 1273 /tissue\_type="brain" /lab\_hos="DH10B" /loone\_lib="LiB3935" /note="Vector: pSPORT1; Site\_1: Sal1; Site\_2: Not1; brain from normal dog" 793 853 973 361 CCTTCCTAGAATCCTTCCTTGTGTCTTTATTCTTATTCTTATTCTTACTGTTTCCTCAACAGTG 541 121 913 181 241 301 421 481 61 734 GGTTGGTGACAGCCGCCTACAACTACTTCCATGTGACCAACTTCTTCTGGATGTTCGGCG 3 GETTGGTGACAGCTGCCTACAACTACTTCCA-GTGACCAACTTCTTCTGGATGTTTGGGG 794 AGGGCTGCTACCTGCACACACACCATCGTGCTCACCTACTCCACTGACCGGCTGCGCAAAT 62 AGGGCTGCTACCTGCACACGGCCATTGTGCTTACCTACTCCACTGACCGGCTGCGCAAGT GGATGTTCATCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCTGGGCCATTG 122 GGATGTTCATCTGCATCGGCTGGGGTGTGCCTTTCCCCATCATCGTGGCCTGGGCCATCG 914 GGAAGCTGTACTACGACAATGAGAAGTGCTGGTTTTGGCAAAAGGCCTGGGGTGTACACCG 974 ACTACATCTACCAGGGCCCCATGATCCTGGTCCTGCTGATCATTTCATCTTTTCA 242 ACTACATCTACCAGGGCCCCATGATCTTGGTCCTGCTGATCAATTTTATCTTTCATTTATC 1034 ACATCGTCCGCATCCTCATGACCAAGCTCCGGGGCATCCACCACGTCTGAGACCATTCAGT 302 ACAICGTCCGCATTCTTATGACCAAACTCCGGGCATCCACCACCACTTCAGT 422 TGTTCTTCGTAAACCCCCGGGAGGACGACGTCTCCCCGGGTCATCTTCATCTACTTCAACT 1094 ACAGGAAGGCTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGCATCACCTACATGC 362 ACAGGAAGGCTGTGAAGGCCACTCTGGTGCTGCTTCCCCTCCTGGGCATCACGTACATGC TGTTCTTCGTCAATCCCGGGGAGGATGAGGTCTCCCCGGGTCGTCTTCATCTACTTCAACT Gaps .. H 581; Length Indels 482 셤 ઠે

1274 AGGTCCGTTCTGCCATCCGGAAGAGGTGGCACCGGTGGCA 1313

RESULT 6 DN396007

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AGENCORT 6649915 NIH MGC_114 Homo sapiens CDNA clone IMAGE:5764209
57, mRNA sequence.
BM925912
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
                                                                                                                       295 TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCAACGCATCCGTGGACCTCATTGGCACC
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.lihl.gov.e. column: 10
                                                                                                                                                                                                                                               GCCGCCCGCGTGAATTACTCCCGAGTGCCAGGAGATCCTCAATGAGGAGAAAAAAGCAAG
                                                                                   TCCCTGGCCAGCAACATCTCAGGACTGCAGTGCAACGCATCCGTGGACCTCATTGGCACC
                                                                                                                                                                                             241 IGCTGGCCCCGCAGCCCTGCGGGCAGCTAGTGGTTCGGCCCTGCCCTGCCTTTTTTCTAT
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
481 CTCCTGGTGGCCTTTGTCCTCTTTCTGCGGCTCAGG 516
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expression library
expression library
/note="Organ: Fetal Brain; Vector: pCMV6-XL4; Site_1:
ECORI; Site_2: XNot/Sall compatible end ligatio; Oligo-dT
primed reverse transcription optimized for large and GC
rich mRNA transcripts, CDNA size selection, optimized
ligation for large inserts into mammalian expression
vector, random clones selected for end sequence
verification of full-length genes"
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E 1 (bases 1 to 727)

S Birkett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L.,
Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M.,
Zhang, X., Jay, G. and He, W.,
High-throughput cloning of full-length human cDNAs directly from cDNA libraries optimized for large and rare transcripts
Unpublished (2005)

L Conteat: Kovacs, KF
High Throughput cDNA Cloning
OriGene Technologies, Inc. ( www.origene.com )

6 Taft Court. Sulte 100, Rockville, MD 20850, USA
Tel: 301 340 3188
                                                                                                                                                                 DR002290
TC110860 Human fetal brain, large insert, pGMV expression library Homo sapiens CDMA clone TC110860 S' similar to Homo sapiens corticotropin releasing hormone receptor 1 (CRHR1), mRNA sequence.
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
6 Taft Ct. Suite 100
Rockville, MD 20850
Tel: (301) 340-3188
http://www.origene.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: pCMV6 Sprime forward vector primer, OriGene Technologies Inc. Location/Qualifiers
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542 AGGTCCGCTCTGCCATCCGGAAGAGGTGGCATCGATGGCA 581
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                         Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCAGGAGATCCTCAATG---AGGAGAAAAAAGCAAGGTGCACTACCATGTCGCAGTCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 29.7%; Score 469.4; DB 10; Length 1176; Best Local Similarity 67.8%; Pred. No. 3.8e-105; Matches 768; Conservative 0; Mismatches 266; Indels 99;
                                                                                                                                                         Location/Qualifiers
1. 1176
Organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                /gene="CRHR2"
/locus_tag="HCM2583"
Adams, M.D. and Cargill, M
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Homo sapiens CRHR2 gene, VINTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
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1 (Dases 1 to 1176)

1 (Dases 1 to 1176)

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,

Ferriars, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,

Adams, M.D. and Cargill, M.
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Homo sapiens
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Givello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
                                                                                                              Gaps
                                                                                                           5
                                                   Length 1148;
                                                                                                           Indels
                                                   Score 491.2; DB 3;
Pred. No. 1.5e-110;
0; Mismatches 33;
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GSS.
                                                   Query Match
Best Local Similarity 93.8%;
Matches 533; Conservative (
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Email: cdna@jgi-psf.org

Insue Procurement: Timothy Grammer (Richard M. Harland Laboratory,
University of California, Berkeley:

http://tropicalis.berkeley.edu/home)

cDNA Library Preparation: DOB Joint Genome Institute:

http://www.jgi.doe.gov

DNA Sequencing: DOB Joint Genome Institute: http://www.jgi.doe.gov

Clone Distribution: I.M.A.G.B. Consortium/LLNL:

http://image.llnl.gov

Naming Conventions: EST name is generated by the concatenation of
the JGI Clone id and the direction of sequencing. The suffix '.fwd'
indicates a forward sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.

Plate: CAAO 0089 row: o column: 1

High quality sequence stop: 818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CX955987 B75 bp mRNA linear BST 08-PEB-2005 JGI CAAO8456.fwd NIH XGC_tropTe5 Xenopus tropicalis cDNA clone IMAGE:7705563 5', mRNA sequence.
                                                             983 ACCAGGGCCCCATGATCCTGGTCCTGCTGATCAATTTCATCTTCCTTTTCAACATCGTCC 1042
                                                                                                                                                                            944 GGATCCTAATGACAAAGTTACGCGCGTCCACACATCCGAGACAATCCAGTACAGGAAGG 1003
                                                                                                                                                                                                                                          1004 CAGTGAAGGCCACCCTGGTGCTCCTGCCCTCCTGGGCATCACCTACATGCTCTTCTTCG 1063
                                                                                                                                                                                                                                                                                                  1043 GCATCCTCATGACCAAGCTCCGGGCATCCACCTCTGAGACCATTCAGTACAGGAAGG 1102
                                                                                                                                                                                                                      CTGTGAAAGCCACTCTGGTGCTGCTGCCCCTCCTGGGCATCACCTACATGCTGTTCTTCG 1162
                                                                                                  884 ACCAAGGCCCCATCATTCTCGGGCTCCTGATCAATTTCGTATTTCTGTTCAACATCATC 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae, Kenopodinae, Kenopus, Silurana.

( Dases 1 to 875)

Richardson, P., Lucas, S., Rokhsar, D., Detter, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.

DOB Joint Genome Institute Kenopus tropicalis EST project
1223 AATCCTTCCAGGGCTTCTTGTGTTCTGTGTTCTACTGTTTCCTCAATAGTGAG 1275
                                                                                                                                                                                                                                                                                                                                                                                                     1124 AGTCGTTCCAGGGTTTCTTCGTGTCTGTCTTCTACTGCTTCTTCAATGGAGAG 1176
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Contact: Lindquist,E.A., Richardson,P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5500
Pax: 925 296 5710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
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/dev_stage="Adult"
/lab_host="ElectroMAX DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:8364"
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AY406516
Pan troglodytes CRHR2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.

AY406516
GSS 15-DEC-2003
AY406516.1 GI:39762490
GSS.
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Pred. No. 4e-105;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Plassaninae; Gallus.

1 (bases 1 to 593)

2 (bases 1 to 593)

3 Matukumalli, L.K. and Van Tassell, C.P.
Characterization of expressed sequence tags generated from multiple
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Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim alt '' -trim fastaVector identified by
cross_match using options -minmatch 12 -minscore 12
Plate: 30 row: M column: 12
Seq primer: CCCAGTCACGACGTTGTAAAACG
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                                                                 551 TGCAGCT---CGTTGACCATGAAGTGCACGAGAGCAATGAGGTCTGGTGCCGCTGCATCA
                                                                                                                                       608 CCACCATCTTCAACTACTTCGTGGTGACCAACTTCTTCTGGATGTTTGTGGGAAGGCTGCT
                                                                                                                                                                                                  ACCTGCACACACCATCGTGCTCACCTACTCCACTGACCGGCTGCGCAAATGGATGCTTCA
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                                                                                                                                                                                                                                                                                      963 TCTGCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCCTGGGCCATTGGGAAGCTGT
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                           TCCAGCTAACCATGAGCCCCCGAGGTCCACCAGAGCAACGTGGGCTGGTGCAGGTTGGTGA
                                                                                                            CAGCCGCCTACAACTACTTCCATGTGACCAACTTCTTCTGGATGTTCGGCGAGGGCTGCT
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Growth Biology Laboratory
Animal and Natural Resources Institute
Bldg. 200 Rm215 BARC-East, Beltsville,
Tel: 3015048224
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Gallus gallus
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                                                                                                                                                                                                                    Inferring nonneutral evolution from human-chimp-mouse orthologous
                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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                                                                               Hominidae, Pan.

1 (bases 1 to 1140)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
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Science 302 (5652), 1960-1963 (2003)
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/locus_tag="HCM2583"
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troglodytes (chimpanzee)
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Best Local Similarity 66.74
Matches 756; Conservative
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Sciurognathi, Muroidea; Muridae; Murinae; Mus.
1 (bases 1 to 1170)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Inferring nonneutral evolution from human-chimp-mouse orthologous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.
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                                                                                                                                                                                                                                                            Science 302 (5652), 1960-1963 (2003)
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/organism="Mus musculus"
/mol type="genomic DNA"
/db_xref="taxon:10090"
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/gene="CRHR2"
/locus_tag="HCM2583"
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                                                                                                                                                                                          /db_xref="caxon:9031"
/clone="304L_30M12"
/lab_host="DH5alpa"
/clone lib="BAGAC_3GAL_chicken mixed tissue"
/clone lib="BAGC_3GAL_chicken mixed tissue"
/note="Vector: pBluescript, SK+, Stratagene; Site_1: Not1;
Site_2: BCORI, Normalized library of pooled RNA isolated
Site_2: BCORI, ultimobranchial gland, parathyroid
gland, cecal tonsil and primordial germ cells Multiple"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  947 TTGGCAAAAGGCCTGGGGTGTACACCGACTACATCTACCAGGCCCCCATGATCCTGGTCC 1006
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            886
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GSS.
Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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Mus musculus CRHR2 gene, VIRTUAL TRANSCRIPT, partial sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29.0%; Score 458.2; DB 7; Length 583; 86.6%; Pred. No. 2e-102; ive 0; Mismatches 78; Indels 0
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                                                                         1. .583
/organlus gallus"
/mol type="mRNA"
/strain="Leghorn and broiler"
         quality sequence stop: 583.
Location/Qualifiers
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nes 505; Conservative
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Matches 505;
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Xenopus tropicalis (western clawed frog)
Kanopus tropicalis
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Kenopodinae; Kenopus; Silurana.
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Matches 487; Conservative
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/lab_host="DH10B"
/clone_lib="CSEQRBN14"
/note="Organ: ovary; Vector: pBluescript II KS(+); Site_1:
                                                                                                                                                                                                                                     986 AGGCCCCATGATCCTGCTGATCAATTTCATCTTCCTTTTCAACATCGTCCGCA 1045
                                                                                                                                                                                                                                                                                                                    1046 TCCTCATGACCAAGCTCCGGGCATCCACCACGTCTGAGACCATTCAGTACAGGAAGGCTG 1105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae; Phasianinae, Gallus.

1 bases 1 to 680)

Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs

Curr. Biol. 12 (22), 1965-1969 (2002)
                                                                                                                                                                                                                                                                                                                                                         941 TCCTGATGACGAAGTTACGAGCATCCACCACGTCCGAGACAATCCAATACAGGAAGGCAG 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                       1001 TGAAGGCCACGCTGGTCCTCCTCCCCTGTTGGGCATCACCTACATGCTCTTTTGTCA 1060
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                      866 GCATTGGCTGGGGTGTGCCCTTCCCCATCATTGTGGCCTGGGCCATTGGGAAGCTGTACT
                                                                                                           761 TCATTGGATGGTGCATTCCCTGCCTATCATCATCGCCTGGGCAGTTGGCAAACTCTACT
                                                                                                                                                                                   881 AGGGCCCGTCATGCTTGTTGTTGATCAATTTTGTATTTCTGTTTAACATCGTCAGGA
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TGCACACACACATCGTGCTCACCTACTCCACTGACCGGCTGCGCAAATGGATGTTCATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
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/organism="Gallus gallus"
/mol type="mRNA"
fstrain="Layer"
/db_xref="teaxon:9031"
/clone="ChEST704a13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Simon. Hubbard@umist.ac.uk.
Location/Qualifiers
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BU454812.1 GI:25944123
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Gallus gallus
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AUTHORS
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PUBMED
COMMENT
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PEATURES

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ECORI; Site 2: Not1; This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with ECORI, size-selected, and cloned into the NotI and ECORI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1966): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CX885516 1inear EST 04-FEB-2005
JGI CAAL23468.fwd NIH XGC tropBrn4 Xenopus tropicalis cDNA clone
IMAGE:7793701 5', mRNA sequence.
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86.2%; Pred. No. 6e-98;
tive 0; Mismatches 78; Indels 0
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Contact: LindquIst, R.A., Richardson, P.
DOB Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: Cahaedjaj-tpsf.org
Tissue Procurement: Timothy Grammer (Richard M. Harland Laboratory, University of California, Berkeley:
http://kropicalis.berkeley.edu/home)
cDNA Library Preparation: DOB Joint Genome Institute:
http://www.jgi.doe.gov
DNA Sequencing: DOB Joint Genome Institute:
clone Distribution: I.M.A.G.B. Consortium/LIME:
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Naming Conventions: EST name is generated by the concatenation of the JGI Clone Id and the direction of sequencing. The suffix '.fwd' indicates a forward sequencing read of the insert. It does not necessarily reflect the oxientation of the insert.

Plate: CAAL 0245 row: g column: 11
High quality sequence stop: 766.

Location/Qualifiers
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    1 (bases 1 to 766)
Richardson,P., Lucas,S., Rokhsar,D., Detter,J.C., Ng,D.C.,
Brokstein,P. and Lindquist,E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
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mol type="manh"
db xref="t-axon.8364"
/clone="IMAGE:7793701"
/fissue_type="Brain"
/dev stage="Adult"
/lab_nost="ElectroMAX DH108"
                                                                                                                    TITLE
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